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(54) Title: HUMAN KINASES

(57) Abstract: The invention provides human kinases (PKIN) and polynucleotides which identify and encode PKIN. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating or prevention disorders associated with aberrant expression of PKIN.



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HUMAN KINASES

TECHNICAL FIELD

This invention relates to nucleic acid and amino acid sequences of human kinases and to the use of these sequences in the diagnosis, treatment, and prevention of cancer, immune disorders, disorders affecting growth and development, cardiovascular diseases, and lipid disorders, and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of human kinases.

BACKGROUND OF THE INVENTION

Kinases comprise the largest known enzyme superfamily and vary widely in their target molecules. Kinases catalyze the transfer of high energy phosphate groups from a phosphate donor to a phosphate acceptor. Nucleotides usually serve as the phosphate donor in these reactions, with most kinases utilizing adenosine triphosphate (ATP). The phosphate acceptor can be any of a variety of molecules, including nucleosides, nucleotides, lipids, carbohydrates, and proteins. Proteins are phosphorylated on hydroxyamino acids. Addition of a phosphate group alters the local charge on the acceptor molecule, causing internal conformational changes and potentially influencing intermolecular contacts. Reversible protein phosphorylation is the primary method for regulating protein activity in eukaryotic cells. In general, proteins are activated by phosphorylation in response to extracellular signals such as hormones, neurotransmitters, and growth and differentiation factors. The activated proteins initiate the cell's intracellular response by way of intracellular signaling pathways and second messenger molecules such as cyclic nucleotides, calcium-calmodulin, inositol, and various mitogens, that regulate protein phosphorylation.

Kinases are involved in all aspects of a cell's function, from basic metabolic processes, such as glycolysis, to cell-cycle regulation, differentiation, and communication with the extracellular environment through signal transduction cascades. Inappropriate phosphorylation of proteins in cells has been linked to changes in cell cycle progression and cell differentiation. Changes in the cell cycle have been linked to induction of apoptosis or cancer. Changes in cell differentiation have been linked to diseases and disorders of the reproductive system, immune system, and skeletal muscle.

There are two classes of protein kinases. One class, protein tyrosine kinases (PTKs), phosphorylates tyrosine residues, and the other class, protein serine/threonine kinases (STKs), phosphorylates serine and threonine residues. Some PTKs and STKs possess structural characteristics of both families and have dual specificity for both tyrosine and serine/threonine residues. Almost all kinases contain a conserved 250-300 amino acid catalytic domain containing specific residues and

sequence motifs characteristic of the kinase family. The protein kinase catalytic domain can be further divided into 11 subdomains. N-terminal subdomains I-IV fold into a two-lobed structure which binds and orients the ATP donor molecule, and subdomain V spans the two lobes. C-terminal subdomains VI-XI bind the protein substrate and transfer the gamma phosphate from ATP to the hydroxyl group of a tyrosine, serine, or threonine residue. Each of the 11 subdomains contains specific catalytic residues or amino acid motifs characteristic of that subdomain. For example, subdomain I contains an 8-amino acid glycine-rich ATP binding consensus motif, subdomain II contains a critical lysine residue required for maximal catalytic activity, and subdomains VI through IX comprise the highly conserved catalytic core. PTKs and STKs also contain distinct sequence motifs in subdomains VI and VIII which may confer hydroxyamino acid specificity.

In addition, kinases may also be classified by additional amino acid sequences, generally between 5 and 100 residues, which either flank or occur within the kinase domain. These additional amino acid sequences regulate kinase activity and determine substrate specificity. (Reviewed in Hardie, G. and S. Hanks (1995) The Protein Kinase Facts Book, Vol I, pp. 17-20 Academic Press, San Diego CA.). In particular, two protein kinase signature sequences have been identified in the kinase domain, the first containing an active site lysine residue involved in ATP binding, and the second containing an aspartate residue important for catalytic activity. If a protein analyzed includes the two protein kinase signatures, the probability of that protein being a protein kinase is close to 100% (PROSITE: PDOC00100, November 1995).

Protein Tyrosine Kinases

Protein tyrosine kinases (PTKs) may be classified as either transmembrane, receptor PTKs or nontransmembrane, nonreceptor PTK proteins. Transmembrane tyrosine kinases function as receptors for most growth factors. Growth factors bind to the receptor tyrosine kinase (RTK), which causes the receptor to phosphorylate itself (autophosphorylation) and specific intracellular second messenger proteins. Growth factors (GF) that associate with receptor PTKs include epidermal GF, platelet-derived GF, fibroblast GF, hepatocyte GF, insulin and insulin-like GFs, nerve GF, vascular endothelial GF, and macrophage colony stimulating factor.

Nontransmembrane, nonreceptor PTKs lack transmembrane regions and, instead, form signaling complexes with the cytosolic domains of plasma membrane receptors. Receptors that function through non-receptor PTKs include those for cytokines and hormones (growth hormone and prolactin), and antigen-specific receptors on T and B lymphocytes.

Many PTKs were first identified as oncogene products in cancer cells in which PTK activation was no longer subject to normal cellular controls. In fact, about one third of the known oncogenes encode PTKs. Furthermore, cellular transformation (oncogenesis) is often accompanied by increased

tyrosine phosphorylation activity (Charbonneau, H. and N.K. Tonks (1992) *Annu. Rev. Cell Biol.* 8:463-493). Regulation of PTK activity may therefore be an important strategy in controlling some types of cancer.

Protein Serine/Threonine Kinases

5 Protein serine/threonine kinases (STKs) are nontransmembrane proteins. A subclass of STKs are known as ERKs (extracellular signal regulated kinases) or MAPs (mitogen-activated protein kinases) and are activated after cell stimulation by a variety of hormones and growth factors. Cell stimulation induces a signaling cascade leading to phosphorylation of MEK (MAP/ERK kinase) which, in turn, activates ERK via serine and threonine phosphorylation. A varied number of proteins represent
10 the downstream effectors for the active ERK and implicate it in the control of cell proliferation and differentiation, as well as regulation of the cytoskeleton. Activation of ERK is normally transient, and cells possess dual specificity phosphatases that are responsible for its down-regulation. Also, numerous studies have shown that elevated ERK activity is associated with some cancers. Other STKs include
15 the second messenger dependent protein kinases such as the cyclic-AMP dependent protein kinases (PKA), calcium-calmodulin (CaM) dependent protein kinases, and the mitogen-activated protein kinases (MAP); the cyclin-dependent protein kinases; checkpoint and cell cycle kinases; Numb-associated kinase (Nak); human Fused (hFu); proliferation-related kinases; 5'-AMP-activated protein kinases; and kinases involved in apoptosis.

The second messenger dependent protein kinases primarily mediate the effects of second
20 messengers such as cyclic AMP (cAMP), cyclic GMP, inositol triphosphate, phosphatidylinositol, 3,4,5-triphosphate, cyclic ADP ribose, arachidonic acid, diacylglycerol and calcium-calmodulin. The PKAs are involved in mediating hormone-induced cellular responses and are activated by cAMP produced within the cell in response to hormone stimulation. cAMP is an intracellular mediator of hormone action in all animal cells that have been studied. Hormone-induced cellular responses
25 include thyroid hormone secretion, cortisol secretion, progesterone secretion, glycogen breakdown, bone resorption, and regulation of heart rate and force of heart muscle contraction. PKA is found in all animal cells and is thought to account for the effects of cAMP in most of these cells. Altered PKA expression is implicated in a variety of disorders and diseases including cancer, thyroid disorders, diabetes, atherosclerosis, and cardiovascular disease (Isselbacher, K.J. et al. (1994) Harrison's
30 Principles of Internal Medicine, McGraw-Hill, New York NY, pp. 416-431, 1887).

The casein kinase I (CKI) gene family is another subfamily of serine/threonine protein kinases. This continuously expanding group of kinases have been implicated in the regulation of numerous cytoplasmic and nuclear processes, including cell metabolism, and DNA replication and repair. CKI enzymes are present in the membranes, nucleus, cytoplasm and cytoskeleton of eukaryotic cells, and on

the mitotic spindles of mammalian cells (Fish, K.J. et al. (1995) J. Biol. Chem. 270:14875-14883).

The CKI family members all have a short amino-terminal domain of 9-76 amino acids, a highly conserved kinase domain of 284 amino acids, and a variable carboxyl-terminal domain that ranges from 24 to over 200 amino acids in length (Cegielska, A. et al. (1998) J. Biol. Chem. 273:1357-1364). The CKI family is comprised of highly related proteins, as seen by the identification of isoforms of casein kinase I from a variety of sources. There are at least five mammalian isoforms, α , β , γ , δ , and ϵ . Fish et al., identified CKI-epsilon from a human placenta cDNA library. It is a basic protein of 416 amino acids and is closest to CKI-delta. Through recombinant expression, it was determined to phosphorylate known CKI substrates and was inhibited by the CKI-specific inhibitor CKI-7. The human gene for CKI-epsilon was able to rescue yeast with a slow-growth phenotype caused by deletion of the yeast CKI locus, HRR250 (Fish et al., *supra*).

The mammalian circadian mutation tau was found to be a semidominant autosomal allele of CKI-epsilon that markedly shortens period length of circadian rhythms in Syrian hamsters. The tau locus is encoded by casein kinase I-epsilon, which is also a homolog of the *Drosophila* circadian gene double-time. Studies of both the wildtype and tau mutant CKI-epsilon enzyme indicated that the mutant enzyme has a noticeable reduction in the maximum velocity and autophosphorylation state. Further, *in vitro*, CKI-epsilon is able to interact with mammalian PERIOD proteins, while the mutant enzyme is deficient in its ability to phosphorylate PERIOD. Lowrey et al., have proposed that CKI-epsilon plays a major role in delaying the negative feedback signal within the transcription-translation-based autoregulatory loop that composes the core of the circadian mechanism. Therefore the CKI-epsilon enzyme is an ideal target for pharmaceutical compounds influencing circadian rhythms, jet-lag and sleep, in addition to other physiologic and metabolic processes under circadian regulation (Lowrey, P.L. et al. (2000) Science 288:483-491).

Homeodomain-interacting protein kinases (HIPKs) are serine/threonine kinases and novel members of the DYRK kinase subfamily (Hofmann, T.G. et al. (2000) Biochimie 82:1123-1127). HIPKs contain a conserved protein kinase domain separated from a domain that interacts with homeoproteins. HIPKs are nuclear kinases, and HIPK2 is highly expressed in neuronal tissue (Kim, Y.H. et al. (1998) J. Biol. Chem. 273:25875-25879; Wang, Y. et al. (2001) Biochim. Biophys. Acta 1518:168-172). HIPKs act as corepressors for homeodomain transcription factors. This corepressor activity is seen in posttranslational modifications such as ubiquitination and phosphorylation, each of which are important in the regulation of cellular protein function (Kim, Y.H. et al. (1999) Proc. Natl. Acad. Sci. USA 96:12350-12355).

Calcium-Calmodulin Dependent Protein Kinases

Calcium-calmodulin dependent (CaM) kinases are involved in regulation of smooth muscle

contraction, glycogen breakdown (phosphorylase kinase), and neurotransmission (CaM kinase I and CaM kinase II). CaM dependent protein kinases are activated by calmodulin, an intracellular calcium receptor, in response to the concentration of free calcium in the cell. Many CaM kinases are also activated by phosphorylation. Some CaM kinases are also activated by autophosphorylation or by other regulatory kinases. CaM kinase I phosphorylates a variety of substrates including the neurotransmitter-related proteins synapsin I and II, the gene transcription regulator, CREB, and the cystic fibrosis conductance regulator protein, CFTR (Haribabu, B. et al. (1995) EMBO J. 14:3679-3686). CaM kinase II also phosphorylates synapsin at different sites and controls the synthesis of catecholamines in the brain through phosphorylation and activation of tyrosine hydroxylase. CaM kinase II controls the synthesis of catecholamines and serotonin, through phosphorylation/activation of tyrosine hydroxylase and tryptophan hydroxylase, respectively (Fujisawa, H. (1990) BioEssays 12:27-29). The mRNA encoding a calmodulin-binding protein kinase-like protein was found to be enriched in mammalian forebrain. This protein is associated with vesicles in both axons and dendrites and accumulates largely postnatally. The amino acid sequence of this protein is similar to CaM-dependent STKs, and the protein binds calmodulin in the presence of calcium (Godbout, M. et al. (1994) J. Neurosci. 14:1-13).

Mitogen-Activated Protein Kinases

The mitogen-activated protein kinases (MAP) which mediate signal transduction from the cell surface to the nucleus via phosphorylation cascades are another STK family that regulates intracellular signaling pathways. Several subgroups have been identified, and each manifests different substrate specificities and responds to distinct extracellular stimuli (Egan, S.E. and R.A. Weinberg (1993) Nature 365:781-783). MAP kinase signaling pathways are present in mammalian cells as well as in yeast. The extracellular stimuli which activate MAP kinase pathways include epidermal growth factor (EGF), ultraviolet light, hyperosmolar medium, heat shock, endotoxic lipopolysaccharide (LPS), and pro-inflammatory cytokines such as tumor necrosis factor (TNF) and interleukin-1 (IL-1). Altered MAP kinase expression is implicated in a variety of disease conditions including cancer, inflammation, immune disorders, and disorders affecting growth and development.

Cyclin-Dependent Protein Kinases

The cyclin-dependent protein kinases (CDKs) are STKs that control the progression of cells through the cell cycle. The entry and exit of a cell from mitosis are regulated by the synthesis and destruction of a family of activating proteins called cyclins. Cyclins are small regulatory proteins that bind to and activate CDKs, which then phosphorylate and activate selected proteins involved in the mitotic process. CDKs are unique in that they require multiple inputs to become activated. In addition to cyclin binding, CDK activation requires the phosphorylation of a specific threonine residue and the

dephosphorylation of a specific tyrosine residue on the CDK.

Another family of STKs associated with the cell cycle are the NIMA (never in mitosis)-related kinases (Neks). Both CDKs and Neks are involved in duplication, maturation, and separation of the microtubule organizing center, the centrosome, in animal cells (Fry, A.M. et al. (1998) EMBO J.

5 17:470-481).

Checkpoint and Cell Cycle Kinases

In the process of cell division, the order and timing of cell cycle transitions are under control of cell cycle checkpoints, which ensure that critical events such as DNA replication and chromosome segregation are carried out with precision. If DNA is damaged, e.g. by radiation, a checkpoint pathway is activated that arrests the cell cycle to provide time for repair. If the damage is extensive, apoptosis is induced. In the absence of such checkpoints, the damaged DNA is inherited by aberrant cells which may cause proliferative disorders such as cancer. Protein kinases play an important role in this process. For example, a specific kinase, checkpoint kinase 1 (Chk1), has been identified in yeast and mammals, and is activated by DNA damage in yeast. Activation of Chk1 leads to the arrest of the cell at the G2/M transition (Sanchez, Y. et al. (1997) Science 277:1497-1501). Specifically, Chk1 phosphorylates the cell division cycle phosphatase CDC25, inhibiting its normal function which is to dephosphorylate and activate the cyclin-dependent kinase Cdc2. Cdc2 activation controls the entry of cells into mitosis (Peng, C.-Y. et al. (1997) Science 277:1501-1505). Thus, activation of Chk1 prevents the damaged cell from entering mitosis. A similar deficiency in a checkpoint kinase, such as Chk1, may also contribute to cancer by failure to arrest cells with damaged DNA at other checkpoints such as G2/M.

Proliferation-Related Kinases

Proliferation-related kinase is a serum/cytokine inducible STK that is involved in regulation of the cell cycle and cell proliferation in human megakaryocytic cells (Li, B. et al. (1996) J. Biol. Chem. 271:19402-19408). Proliferation-related kinase is related to the polo (derived from *Drosophila* polo gene) family of STKs implicated in cell division. Proliferation-related kinase is downregulated in lung tumor tissue and may be a proto-oncogene whose deregulated expression in normal tissue leads to oncogenic transformation.

5'-AMP-activated protein kinase

A ligand-activated STK protein kinase is 5'-AMP-activated protein kinase (AMPK) (Gao, G. et al. (1996) J. Biol Chem. 271:8675-8681). Mammalian AMPK is a regulator of fatty acid and sterol synthesis through phosphorylation of the enzymes acetyl-CoA carboxylase and hydroxymethylglutaryl-CoA reductase and mediates responses of these pathways to cellular stresses such as heat shock and depletion of glucose and ATP. AMPK is a heterotrimeric complex comprised of

a catalytic alpha subunit and two non-catalytic beta and gamma subunits that are believed to regulate the activity of the alpha subunit. Subunits of AMPK have a much wider distribution in non-lipogenic tissues such as brain, heart, spleen, and lung than expected. This distribution suggests that its role may extend beyond regulation of lipid metabolism alone.

5 Kinases in Apoptosis

Apoptosis is a highly regulated signaling pathway leading to cell death that plays a crucial role in tissue development and homeostasis. Deregulation of this process is associated with the pathogenesis of a number of diseases including autoimmune disease, neurodegenerative disorders, and cancer.

Various STKs play key roles in this process. ZIP kinase is an STK containing a C-terminal leucine zipper domain in addition to its N-terminal protein kinase domain. This C-terminal domain appears to mediate homodimerization and activation of the kinase as well as interactions with transcription factors such as activating transcription factor, ATF4, a member of the cyclic-AMP responsive element binding protein (ATF/CREB) family of transcriptional factors (Sanjo, H. et al. (1998) J. Biol. Chem. 273:29066-29071). DRAK1 and DRAK2 are STKs that share homology with the death-associated protein kinases (DAP kinases), known to function in interferon- γ induced apoptosis (Sanjo et al., 15 supra). Like ZIP kinase, DAP kinases contain a C-terminal protein-protein interaction domain, in the form of ankyrin repeats, in addition to the N-terminal kinase domain. ZIP, DAP, and DRAK kinases induce morphological changes associated with apoptosis when transfected into NIH3T3 cells (Sanjo et al., supra). However, deletion of either the N-terminal kinase catalytic domain or the C-terminal 20 domain of these proteins abolishes apoptosis activity, indicating that in addition to the kinase activity, activity in the C-terminal domain is also necessary for apoptosis, possibly as an interacting domain with a regulator or a specific substrate.

RICK is another STK recently identified as mediating a specific apoptotic pathway involving the death receptor, CD95 (Inohara, N. et al. (1998) J. Biol. Chem. 273:12296-12300). CD95 is a 25 member of the tumor necrosis factor receptor superfamily and plays a critical role in the regulation and homeostasis of the immune system (Nagata, S. (1997) Cell 88:355-365). The CD95 receptor signaling pathway involves recruitment of various intracellular molecules to a receptor complex following ligand binding. This process includes recruitment of the cysteine protease caspase-8 which, in turn, activates a caspase cascade leading to cell death. RICK is composed of an N-terminal kinase catalytic domain and 30 a C-terminal "caspase-recruitment" domain that interacts with caspase-like domains, indicating that RICK plays a role in the recruitment of caspase-8. This interpretation is supported by the fact that the expression of RICK in human 293T cells promotes activation of caspase-8 and potentiates the induction of apoptosis by various proteins involved in the CD95 apoptosis pathway (Inohara et al., supra).

Mitochondrial Protein Kinases

A novel class of eukaryotic kinases, related by sequence to prokaryotic histidine protein kinases, are the mitochondrial protein kinases (MPKs) which seem to have no sequence similarity with other eukaryotic protein kinases. These protein kinases are located exclusively in the mitochondrial matrix space and may have evolved from genes originally present in respiration-dependent bacteria which were endocytosed by primitive eukaryotic cells. MPKs are responsible for phosphorylation and inactivation of the branched-chain alpha-ketoacid dehydrogenase and pyruvate dehydrogenase complexes (Harris, R.A. et al. (1995) *Adv. Enzyme Regul.* 34:147-162). Five MPKs have been identified. Four members correspond to pyruvate dehydrogenase kinase isozymes, regulating the activity of the pyruvate dehydrogenase complex, which is an important regulatory enzyme at the interface between glycolysis and the citric acid cycle. The fifth member corresponds to a branched-chain alpha-ketoacid dehydrogenase kinase, important in the regulation of the pathway for the disposal of branched-chain amino acids. (Harris, R.A. et al. (1997) *Adv. Enzyme Regul.* 37:271-293). Both starvation and the diabetic state are known to result in a great increase in the activity of the pyruvate dehydrogenase kinase in the liver, heart and muscle of the rat. This increase contributes in both disease states to the phosphorylation and inactivation of the pyruvate dehydrogenase complex and conservation of pyruvate and lactate for gluconeogenesis (Harris (1995) *supra*).

KINASES WITH NON-PROTEIN SUBSTRATES

20 Lipid and Inositol kinases

Lipid kinases phosphorylate hydroxyl residues on lipid head groups. A family of kinases involved in phosphorylation of phosphatidylinositol (PI) has been described, each member phosphorylating a specific carbon on the inositol ring (Leevers, S.J. et al. (1999) *Curr. Opin. Cell. Biol.* 11:219-225). The phosphorylation of phosphatidylinositol is involved in activation of the protein kinase C signaling pathway. The inositol phospholipids (phosphoinositides) intracellular signaling pathway begins with binding of a signaling molecule to a G-protein linked receptor in the plasma membrane. This leads to the phosphorylation of phosphatidylinositol (PI) residues on the inner side of the plasma membrane by inositol kinases, thus converting PI residues to the biphosphate state (PIP₂). PIP₂ is then cleaved into inositol triphosphate (IP₃) and diacylglycerol. These two products act as mediators for separate signaling pathways. Cellular responses that are mediated by these pathways are glycogen breakdown in the liver in response to vasopressin, smooth muscle contraction in response to acetylcholine, and thrombin-induced platelet aggregation.

PI 3-kinase (PI3K), which phosphorylates the D3 position of PI and its derivatives, has a central role in growth factor signal cascades involved in cell growth, differentiation, and metabolism.

PI3K is a heterodimer consisting of an adapter subunit and a catalytic subunit. The adapter subunit acts as a scaffolding protein, interacting with specific tyrosine-phosphorylated proteins, lipid moieties, and other cytosolic factors. When the adapter subunit binds tyrosine phosphorylated targets, such as the insulin responsive substrate (IRS)-1, the catalytic subunit is activated and converts PI (4,5)

5 bisphosphate (PIP₂) to PI (3,4,5) P₃ (PIP₃). PIP₃ then activates a number of other proteins, including PKA, protein kinase B (PKB), protein kinase C (PKC), glycogen synthase kinase (GSK)-3, and p70 ribosomal s6 kinase. PI3K also interacts directly with the cytoskeletal organizing proteins, Rac, rho, and cdc42 (Shepherd, P.R. et al. (1998) Biochem. J. 333:471-490). Animal models for diabetes, such as *obese* and *fat* mice, have altered PI3K adapter subunit levels. Specific mutations in the adapter
10 subunit have also been found in an insulin-resistant Danish population, suggesting a role for PI3K in type-2 diabetes (Shepard, supra).

An example of lipid kinase phosphorylation activity is the phosphorylation of D-erythro-sphingosine to the sphingolipid metabolite, sphingosine-1-phosphate (SPP). SPP has emerged as a novel lipid second-messenger with both extracellular and intracellular actions (Kohama,
15 T. et al. (1998) J. Biol. Chem. 273:23722-23728). Extracellularly, SPP is a ligand for the G-protein coupled receptor EDG-1 (endothelial-derived, G-protein coupled receptor). Intracellularly, SPP regulates cell growth, survival, motility, and cytoskeletal changes. SPP levels are regulated by sphingosine kinases that specifically phosphorylate D-erythro-sphingosine to SPP. The importance of sphingosine kinase in cell signaling is indicated by the fact that various stimuli, including
20 platelet-derived growth factor (PDGF), nerve growth factor, and activation of protein kinase C, increase cellular levels of SPP by activation of sphingosine kinase, and the fact that competitive inhibitors of the enzyme selectively inhibit cell proliferation induced by PDGF (Kohama et al., supra).

Purine Nucleotide Kinases

The purine nucleotide kinases, adenylate kinase (ATP:AMP phosphotransferase, or AdK) and
25 guanylate kinase (ATP:GMP phosphotransferase, or GuK) play a key role in nucleotide metabolism and are crucial to the synthesis and regulation of cellular levels of ATP and GTP, respectively. These two molecules are precursors in DNA and RNA synthesis in growing cells and provide the primary source of biochemical energy in cells (ATP), and signal transduction pathways (GTP). Inhibition of various steps in the synthesis of these two molecules has been the basis of many antiproliferative drugs for
30 cancer and antiviral therapy (Pillwein, K. et al. (1990) Cancer Res. 50:1576-1579).

AdK is found in almost all cell types and is especially abundant in cells having high rates of ATP synthesis and utilization such as skeletal muscle. In these cells AdK is physically associated with mitochondria and myofibrils, the subcellular structures that are involved in energy production and utilization, respectively. Recent studies have demonstrated a major function for AdK in transferring

high energy phosphoryls from metabolic processes generating ATP to cellular components consuming ATP (Zelevnikar, R.J. et al. (1995) J. Biol. Chem. 270:7311-7319). Thus AdK may have a pivotal role in maintaining energy production in cells, particularly those having a high rate of growth or metabolism such as cancer cells, and may provide a target for suppression of its activity to treat certain cancers.

- 5 Alternatively, reduced AdK activity may be a source of various metabolic, muscle-energy disorders that can result in cardiac or respiratory failure and may be treatable by increasing AdK activity.

GuK, in addition to providing a key step in the synthesis of GTP for RNA and DNA synthesis, also fulfills an essential function in signal transduction pathways of cells through the regulation of GDP and GTP. Specifically, GTP binding to membrane associated G proteins mediates the activation of cell
10 receptors, subsequent intracellular activation of adenylyl cyclase, and production of the second messenger, cyclic AMP. GDP binding to G proteins inhibits these processes. GDP and GTP levels also control the activity of certain oncogenic proteins such as p21^{ras} known to be involved in control of cell proliferation and oncogenesis (Bos, J.L. (1989) Cancer Res. 49:4682-4689). High ratios of GTP:GDP caused by suppression of GuK cause activation of p21^{ras} and promote oncogenesis.
15 Increasing GuK activity to increase levels of GDP and reduce the GTP:GDP ratio may provide a therapeutic strategy to reverse oncogenesis.

GuK is an important enzyme in the phosphorylation and activation of certain antiviral drugs useful in the treatment of herpes virus infections. These drugs include the guanine homologs acyclovir and bucciclovir (Miller, W.H. and R.L. Miller (1980) J. Biol. Chem. 255:7204-7207; Stenberg, K. et al.
20 (1986) J. Biol. Chem. 261:2134-2139). Increasing GuK activity in infected cells may provide a therapeutic strategy for augmenting the effectiveness of these drugs and possibly for reducing the necessary dosages of the drugs.

Pyrimidine Kinases

The pyrimidine kinases are deoxycytidine kinase and thymidine kinase 1 and 2. Deoxycytidine
25 kinase is located in the nucleus, and thymidine kinase 1 and 2 are found in the cytosol (Johansson, M. et al. (1997) Proc. Natl. Acad. Sci. USA 94:11941-11945). Phosphorylation of deoxyribonucleosides by pyrimidine kinases provides an alternative pathway for de novo synthesis of DNA precursors. The role of pyrimidine kinases, like purine kinases, in phosphorylation is critical to the activation of several chemotherapeutically important nucleoside analogues (Arner E.S. and S. Eriksson (1995) Pharmacol.
30 Ther. 67:155-186).

The discovery of new human kinases and the polynucleotides encoding them satisfies a need in the art by providing new compositions which are useful in the diagnosis, prevention, and treatment of cancer, immune disorders, disorders affecting growth and development, cardiovascular diseases, and lipid disorders, and in the assessment of the effects of exogenous compounds on the expression of

nucleic acid and amino acid sequences of human kinases.

SUMMARY OF THE INVENTION

The invention features purified polypeptides, human kinases, referred to collectively as "PKIN" and individually as "PKIN-1," "PKIN-2," "PKIN-3," "PKIN-4," "PKIN-5," "PKIN-6," "PKIN-7," "PKIN-8," "PKIN-9," "PKIN-10," "PKIN-11," "PKIN-12," "PKIN-13," "PKIN-14," "PKIN-15," "PKIN-16," "PKIN-17," "PKIN-18," "PKIN-19," "PKIN-20," "PKIN-21," "PKIN-22," "PKIN-23," "PKIN-24," "PKIN-25," and "PKIN-26." In one aspect, the invention provides an isolated polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26. In one alternative, the invention provides an isolated polypeptide comprising the amino acid sequence of SEQ ID NO:1-26.

The invention further provides an isolated polynucleotide encoding a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26. In one alternative, the polynucleotide encodes a polypeptide selected from the group consisting of SEQ ID NO:1-26. In another alternative, the polynucleotide is selected from the group consisting of SEQ ID NO:27-52.

Additionally, the invention provides a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26. In one alternative, the invention provides a cell transformed with the recombinant polynucleotide. In another alternative, the invention provides a

transgenic organism comprising the recombinant polynucleotide.

The invention also provides a method for producing a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26. The method comprises a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding the polypeptide, and b) recovering the polypeptide so expressed.

Additionally, the invention provides an isolated antibody which specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26.

The invention further provides an isolated polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:27-52, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:27-52, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). In one alternative, the polynucleotide comprises at least 60 contiguous nucleotides.

Additionally, the invention provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:27-52, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:27-52, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). The method comprises a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to

said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and b) detecting the presence or absence of said hybridization complex, and optionally, if present, the amount thereof. In one alternative, the probe comprises at least 60 contiguous nucleotides.

5 The invention further provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:27-52, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:27-52, c) a
10 polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). The method comprises a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

15 The invention further provides a composition comprising an effective amount of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, c) a biologically active fragment of a polypeptide having an amino acid sequence selected
20 from the group consisting of SEQ ID NO:1-26, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, and a pharmaceutically acceptable excipient. In one embodiment, the composition comprises an amino acid sequence selected from the group consisting of SEQ ID NO:1-26. The invention additionally provides a method of treating a disease or condition associated with decreased expression of functional PKIN, comprising administering to a patient in need of such treatment the composition.
25

 The invention also provides a method for screening a compound for effectiveness as an agonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from
30 the group consisting of SEQ ID NO:1-26, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting agonist activity in the sample. In one alternative, the invention provides a

composition comprising an agonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with decreased expression of functional PKIN, comprising administering to a patient in need of such treatment the composition.

5 Additionally, the invention provides a method for screening a compound for effectiveness as an antagonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, c) a biologically active fragment of a
10 polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting antagonist activity in the sample. In one alternative, the invention provides a composition comprising an antagonist compound identified by the method and a
15 pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with overexpression of functional PKIN, comprising administering to a patient in need of such treatment the composition.

 The invention further provides a method of screening for a compound that specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid
20 sequence selected from the group consisting of SEQ ID NO:1-26, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, and d) an immunogenic
25 fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26. The method comprises a) combining the polypeptide with at least one test compound under suitable conditions, and b) detecting binding of the polypeptide to the test compound, thereby identifying a compound that specifically binds to the polypeptide.

 The invention further provides a method of screening for a compound that modulates the activity of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino
30 acid sequence selected from the group consisting of SEQ ID NO:1-26, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, and d) an immunogenic
fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID

NO:1-26. The method comprises a) combining the polypeptide with at least one test compound under conditions permissive for the activity of the polypeptide, b) assessing the activity of the polypeptide in the presence of the test compound, and c) comparing the activity of the polypeptide in the presence of the test compound with the activity of the polypeptide in the absence of the test compound,
 5 wherein a change in the activity of the polypeptide in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide.

The invention further provides a method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence selected from the group consisting of SEQ ID NO:27-52, the method comprising a)
 10 exposing a sample comprising the target polynucleotide to a compound, and b) detecting altered expression of the target polynucleotide.

The invention further provides a method for assessing toxicity of a test compound, said method comprising a) treating a biological sample containing nucleic acids with the test compound; b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20
 15 contiguous nucleotides of a polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:27-52, ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:27-52, iii) a polynucleotide having a sequence complementary to i), iv) a polynucleotide complementary to the
 20 polynucleotide of ii), and v) an RNA equivalent of i)-iv). Hybridization occurs under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:27-52, ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90%
 25 identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:27-52, iii) a polynucleotide complementary to the polynucleotide of i), iv) a polynucleotide complementary to the polynucleotide of ii), and v) an RNA equivalent of i)-iv). Alternatively, the target polynucleotide comprises a fragment of a polynucleotide sequence selected from the group consisting of i)-v) above; c) quantifying the amount of hybridization complex; and d) comparing the amount of hybridization
 30 complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

BRIEF DESCRIPTION OF THE TABLES

35 Table 1 summarizes the nomenclature for the full length polynucleotide and polypeptide

sequences of the present invention.

Table 2 shows the GenBank identification number and annotation of the nearest GenBank homolog for polypeptides of the invention. The probability score for the match between each polypeptide and its GenBank homolog is also shown.

5 Table 3 shows structural features of polypeptide sequences of the invention, including predicted motifs and domains, along with the methods, algorithms, and searchable databases used for analysis of the polypeptides.

Table 4 lists the cDNA and/or genomic DNA fragments which were used to assemble polynucleotide sequences of the invention, along with selected fragments of the polynucleotide
10 sequences.

Table 5 shows the representative cDNA library for polynucleotides of the invention.

Table 6 provides an appendix which describes the tissues and vectors used for construction of the cDNA libraries shown in Table 5.

Table 7 shows the tools, programs, and algorithms used to analyze the polynucleotides and
15 polypeptides of the invention, along with applicable descriptions, references, and threshold parameters.

DESCRIPTION OF THE INVENTION

Before the present proteins, nucleotide sequences, and methods are described, it is understood that this invention is not limited to the particular machines, materials and methods described, as these
20 may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a
25 reference to "a host cell" includes a plurality of such host cells, and a reference to "an antibody" is a reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this invention belongs. Although
30 any machines, materials, and methods similar or equivalent to those described herein can be used to practice or test the present invention, the preferred machines, materials and methods are now described. All publications mentioned herein are cited for the purpose of describing and disclosing the cell lines, protocols, reagents and vectors which are reported in the publications and which might be used in connection with the invention. Nothing herein is to be construed as an admission that the invention is

not entitled to antedate such disclosure by virtue of prior invention.

DEFINITIONS

“PKIN” refers to the amino acid sequences of substantially purified PKIN obtained from any species, particularly a mammalian species, including bovine, ovine, porcine, murine, equine, and human, and from any source, whether natural, synthetic, semi-synthetic, or recombinant.

The term “agonist” refers to a molecule which intensifies or mimics the biological activity of PKIN. Agonists may include proteins, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of PKIN either by directly interacting with PKIN or by acting on components of the biological pathway in which PKIN participates.

An “allelic variant” is an alternative form of the gene encoding PKIN. Allelic variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. A gene may have none, one, or many allelic variants of its naturally occurring form. Common mutational changes which give rise to allelic variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

“Altered” nucleic acid sequences encoding PKIN include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polypeptide the same as PKIN or a polypeptide with at least one functional characteristic of PKIN. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding PKIN, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding PKIN. The encoded protein may also be “altered,” and may contain deletions, insertions, or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent PKIN. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of PKIN is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, and positively charged amino acids may include lysine and arginine. Amino acids with uncharged polar side chains having similar hydrophilicity values may include: asparagine and glutamine; and serine and threonine. Amino acids with uncharged side chains having similar hydrophilicity values may include: leucine, isoleucine, and valine; glycine and alanine; and phenylalanine and tyrosine.

The terms “amino acid” and “amino acid sequence” refer to an oligopeptide, peptide, polypeptide, or protein sequence, or a fragment of any of these, and to naturally occurring or synthetic

molecules. Where "amino acid sequence" is recited to refer to a sequence of a naturally occurring protein molecule, "amino acid sequence" and like terms are not meant to limit the amino acid sequence to the complete native amino acid sequence associated with the recited protein molecule.

"Amplification" relates to the production of additional copies of a nucleic acid sequence.

5 Amplification is generally carried out using polymerase chain reaction (PCR) technologies well known in the art.

The term "antagonist" refers to a molecule which inhibits or attenuates the biological activity of PKIN. Antagonists may include proteins such as antibodies, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of PKIN either by
10 directly interacting with PKIN or by acting on components of the biological pathway in which PKIN participates.

The term "antibody" refers to intact immunoglobulin molecules as well as to fragments thereof, such as Fab, F(ab')₂, and Fv fragments, which are capable of binding an epitopic determinant. Antibodies that bind PKIN polypeptides can be prepared using intact polypeptides or using fragments
15 containing small peptides of interest as the immunizing antigen. The polypeptide or oligopeptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

20 The term "antigenic determinant" refers to that region of a molecule (i.e., an epitope) that makes contact with a particular antibody. When a protein or a fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to antigenic determinants (particular regions or three-dimensional structures on the protein). An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to
25 elicit the immune response) for binding to an antibody.

The term "antisense" refers to any composition capable of base-pairing with the "sense" (coding) strand of a specific nucleic acid sequence. Antisense compositions may include DNA; RNA; peptide nucleic acid (PNA); oligonucleotides having modified backbone linkages such as phosphorothioates, methylphosphonates, or benzylphosphonates; oligonucleotides having modified
30 sugar groups such as 2'-methoxyethyl sugars or 2'-methoxyethoxy sugars; or oligonucleotides having modified bases such as 5-methyl cytosine, 2'-deoxyuracil, or 7-deaza-2'-deoxyguanosine. Antisense molecules may be produced by any method including chemical synthesis or transcription. Once introduced into a cell, the complementary antisense molecule base-pairs with a naturally occurring nucleic acid sequence produced by the cell to form duplexes which block either transcription or

translation. The designation “negative” or “minus” can refer to the antisense strand, and the designation “positive” or “plus” can refer to the sense strand of a reference DNA molecule.

The term “biologically active” refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, “immunologically active” or “immunogenic” refers to the capability of the natural, recombinant, or synthetic PKIN, or of any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

“Complementary” describes the relationship between two single-stranded nucleic acid sequences that anneal by base-pairing. For example, 5'-AGT-3' pairs with its complement, 3'-TCA-5'.

A “composition comprising a given polynucleotide sequence” and a “composition comprising a given amino acid sequence” refer broadly to any composition containing the given polynucleotide or amino acid sequence. The composition may comprise a dry formulation or an aqueous solution. Compositions comprising polynucleotide sequences encoding PKIN or fragments of PKIN may be employed as hybridization probes. The probes may be stored in freeze-dried form and may be associated with a stabilizing agent such as a carbohydrate. In hybridizations, the probe may be deployed in an aqueous solution containing salts (e.g., NaCl), detergents (e.g., sodium dodecyl sulfate; SDS), and other components (e.g., Denhardt's solution, dry milk, salmon sperm DNA, etc.).

“Consensus sequence” refers to a nucleic acid sequence which has been subjected to repeated DNA sequence analysis to resolve uncalled bases, extended using the XL-PCR kit (Applied Biosystems, Foster City CA) in the 5' and/or the 3' direction, and resequenced, or which has been assembled from one or more overlapping cDNA, EST, or genomic DNA fragments using a computer program for fragment assembly, such as the GELVIEW fragment assembly system (GCG, Madison WI) or Phrap (University of Washington, Seattle WA). Some sequences have been both extended and assembled to produce the consensus sequence.

“Conservative amino acid substitutions” are those substitutions that are predicted to least interfere with the properties of the original protein, i.e., the structure and especially the function of the protein is conserved and not significantly changed by such substitutions. The table below shows amino acids which may be substituted for an original amino acid in a protein and which are regarded as conservative amino acid substitutions.

	Original Residue	Conservative Substitution
	Ala	Gly, Ser
	Arg	His, Lys
	Asn	Asp, Gln, His
	Asp	Asn, Glu
	Cys	Ala, Ser
	Gln	Asn, Glu, His

	Glu	Asp, Gln, His
	Gly	Ala
	His	Asn, Arg, Gln, Glu
	Ile	Leu, Val
5	Leu	Ile, Val
	Lys	Arg, Gln, Glu
	Met	Leu, Ile
	Phe	His, Met, Leu, Trp, Tyr
	Ser	Cys, Thr
10	Thr	Ser, Val
	Trp	Phe, Tyr
	Tyr	His, Phe, Trp
	Val	Ile, Leu, Thr

15 Conservative amino acid substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or hydrophobicity of the molecule at the site of the substitution, and/or (c) the bulk of the side chain.

20 A "deletion" refers to a change in the amino acid or nucleotide sequence that results in the absence of one or more amino acid residues or nucleotides.

 The term "derivative" refers to a chemically modified polynucleotide or polypeptide. Chemical modifications of a polynucleotide can include, for example, replacement of hydrogen by an alkyl, acyl, hydroxyl, or amino group. A derivative polynucleotide encodes a polypeptide which retains at least one biological or immunological function of the natural molecule. A derivative polypeptide is one modified
25 by glycosylation, pegylation, or any similar process that retains at least one biological or immunological function of the polypeptide from which it was derived.

 A "detectable label" refers to a reporter molecule or enzyme that is capable of generating a measurable signal and is covalently or noncovalently joined to a polynucleotide or polypeptide.

30 "Differential expression" refers to increased or upregulated; or decreased, downregulated, or absent gene or protein expression, determined by comparing at least two different samples. Such comparisons may be carried out between, for example, a treated and an untreated sample, or a diseased and a normal sample.

 A "fragment" is a unique portion of PKIN or the polynucleotide encoding PKIN which is identical in sequence to but shorter in length than the parent sequence. A fragment may comprise up
35 to the entire length of the defined sequence, minus one nucleotide/amino acid residue. For example, a fragment may comprise from 5 to 1000 contiguous nucleotides or amino acid residues. A fragment used as a probe, primer, antigen, therapeutic molecule, or for other purposes, may be at least 5, 10, 15, 16, 20, 25, 30, 40, 50, 60, 75, 100, 150, 250 or at least 500 contiguous nucleotides or amino acid residues in length. Fragments may be preferentially selected from certain regions of a molecule. For

example, a polypeptide fragment may comprise a certain length of contiguous amino acids selected from the first 250 or 500 amino acids (or first 25% or 50%) of a polypeptide as shown in a certain defined sequence. Clearly these lengths are exemplary, and any length that is supported by the specification, including the Sequence Listing, tables, and figures, may be encompassed by the present
5 embodiments.

A fragment of SEQ ID NO:27-52 comprises a region of unique polynucleotide sequence that specifically identifies SEQ ID NO:27-52, for example, as distinct from any other sequence in the genome from which the fragment was obtained. A fragment of SEQ ID NO:27-52 is useful, for example, in hybridization and amplification technologies and in analogous methods that distinguish
10 SEQ ID NO:27-52 from related polynucleotide sequences. The precise length of a fragment of SEQ ID NO:27-52 and the region of SEQ ID NO:27-52 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A fragment of SEQ ID NO:1-26 is encoded by a fragment of SEQ ID NO:27-52. A fragment of SEQ ID NO:1-26 comprises a region of unique amino acid sequence that specifically identifies
15 SEQ ID NO:1-26. For example, a fragment of SEQ ID NO:1-26 is useful as an immunogenic peptide for the development of antibodies that specifically recognize SEQ ID NO:1-26. The precise length of a fragment of SEQ ID NO:1-26 and the region of SEQ ID NO:1-26 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

20 A "full length" polynucleotide sequence is one containing at least a translation initiation codon (e.g., methionine) followed by an open reading frame and a translation termination codon. A "full length" polynucleotide sequence encodes a "full length" polypeptide sequence.

"Homology" refers to sequence similarity or, interchangeably, sequence identity, between two or more polynucleotide sequences or two or more polypeptide sequences.

25 The terms "percent identity" and "% identity," as applied to polynucleotide sequences, refer to the percentage of residue matches between at least two polynucleotide sequences aligned using a standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way, gaps in the sequences being compared in order to optimize alignment between two sequences, and therefore achieve a more meaningful comparison of the two sequences.

30 Percent identity between polynucleotide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program. This program is part of the LASERGENE software package, a suite of molecular biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in Higgins, D.G. and P.M. Sharp (1989) CABIOS 5:151-153 and in Higgins, D.G. et al. (1992) CABIOS 8:189-191.

For pairwise alignments of polynucleotide sequences, the default parameters are set as follows:

Ktuple=2, gap penalty=5, window=4, and "diagonals saved"=4. The "weighted" residue weight table is selected as the default. Percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polynucleotide sequences.

Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at

<http://www.ncbi.nlm.nih.gov/BLAST/>. The BLAST software suite includes various sequence analysis

programs including "blastn," that is used to align a known polynucleotide sequence with other polynucleotide sequences from a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at <http://www.ncbi.nlm.nih.gov/gorf/bl2.html>. The "BLAST 2 Sequences" tool can be used for both blastn and blastp (discussed below). BLAST

programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the "BLAST 2 Sequences" tool Version 2.0.12 (April-21-2000) set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Reward for match: 1

Penalty for mismatch: -2

Open Gap: 5 and Extension Gap: 2 penalties

Gap x drop-off: 50

Expect: 10

Word Size: 11

Filter: on

Percent identity may be measured over the length of an entire defined sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined sequence, for instance, a fragment of at least 20, at least 30, at least 40, at least 50, at least 70, at least 100, or at least 200 contiguous nucleotides. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures, or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences due to the degeneracy of the genetic code. It is understood that changes in

a nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

The phrases “percent identity” and “% identity,” as applied to polypeptide sequences, refer to the percentage of residue matches between at least two polypeptide sequences aligned using a standardized algorithm. Methods of polypeptide sequence alignment are well-known. Some alignment methods take into account conservative amino acid substitutions. Such conservative substitutions, explained in more detail above, generally preserve the charge and hydrophobicity at the site of substitution, thus preserving the structure (and therefore function) of the polypeptide.

Percent identity between polypeptide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program (described and referenced above). For pairwise alignments of polypeptide sequences using CLUSTAL V, the default parameters are set as follows: Ktuple=1, gap penalty=3, window=5, and “diagonals saved”=5. The PAM250 matrix is selected as the default residue weight table. As with polynucleotide alignments, the percent identity is reported by CLUSTAL V as the “percent similarity” between aligned polypeptide sequence pairs.

Alternatively the NCBI BLAST software suite may be used. For example, for a pairwise comparison of two polypeptide sequences, one may use the “BLAST 2 Sequences” tool Version 2.0.12 (April-21-2000) with blastp set at default parameters. Such default parameters may be, for example:

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Open Gap: 11 and Extension Gap: 1 penalties

Gap x drop-off: 50

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Percent identity may be measured over the length of an entire defined polypeptide sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

“Human artificial chromosomes” (HACs) are linear microchromosomes which may contain DNA sequences of about 6 kb to 10 Mb in size and which contain all of the elements required for chromosome replication, segregation and maintenance.

The term "humanized antibody" refers to an antibody molecule in which the amino acid sequence in the non-antigen binding regions has been altered so that the antibody more closely resembles a human antibody, and still retains its original binding ability.

"Hybridization" refers to the process by which a polynucleotide strand anneals with a complementary strand through base pairing under defined hybridization conditions. Specific hybridization is an indication that two nucleic acid sequences share a high degree of complementarity. Specific hybridization complexes form under permissive annealing conditions and remain hybridized after the "washing" step(s). The washing step(s) is particularly important in determining the stringency of the hybridization process, with more stringent conditions allowing less non-specific binding, i.e., binding between pairs of nucleic acid strands that are not perfectly matched. Permissive conditions for annealing of nucleic acid sequences are routinely determinable by one of ordinary skill in the art and may be consistent among hybridization experiments, whereas wash conditions may be varied among experiments to achieve the desired stringency, and therefore hybridization specificity. Permissive annealing conditions occur, for example, at 68°C in the presence of about 6 x SSC, about 1% (w/v) SDS, and about 100 µg/ml sheared, denatured salmon sperm DNA.

Generally, stringency of hybridization is expressed, in part, with reference to the temperature under which the wash step is carried out. Such wash temperatures are typically selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. An equation for calculating T_m and conditions for nucleic acid hybridization are well known and can be found in Sambrook, J. et al. (1989) Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; specifically see volume 2, chapter 9.

High stringency conditions for hybridization between polynucleotides of the present invention include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS, for 1 hour. Alternatively, temperatures of about 65°C, 60°C, 55°C, or 42°C may be used. SSC concentration may be varied from about 0.1 to 2 x SSC, with SDS being present at about 0.1%. Typically, blocking reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, sheared and denatured salmon sperm DNA at about 100-200 µg/ml. Organic solvent, such as formamide at a concentration of about 35-50% v/v, may also be used under particular circumstances, such as for RNA:DNA hybridizations. Useful variations on these wash conditions will be readily apparent to those of ordinary skill in the art. Hybridization, particularly under high stringency conditions, may be suggestive of evolutionary similarity between the nucleotides. Such similarity is strongly indicative of a similar role for the nucleotides and their encoded polypeptides.

The term "hybridization complex" refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary bases. A hybridization complex may be formed in solution (e.g., C₀t or R₀t analysis) or formed between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g.,
5 paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate to which cells or their nucleic acids have been fixed).

The words "insertion" and "addition" refer to changes in an amino acid or nucleotide sequence resulting in the addition of one or more amino acid residues or nucleotides, respectively.

"Immune response" can refer to conditions associated with inflammation, trauma, immune
10 disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

An "immunogenic fragment" is a polypeptide or oligopeptide fragment of PKIN which is capable of eliciting an immune response when introduced into a living organism, for example, a
15 mammal. The term "immunogenic fragment" also includes any polypeptide or oligopeptide fragment of PKIN which is useful in any of the antibody production methods disclosed herein or known in the art.

The term "microarray" refers to an arrangement of a plurality of polynucleotides, polypeptides, or other chemical compounds on a substrate.

The terms "element" and "array element" refer to a polynucleotide, polypeptide, or other
20 chemical compound having a unique and defined position on a microarray.

The term "modulate" refers to a change in the activity of PKIN. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of PKIN.

The phrases "nucleic acid" and "nucleic acid sequence" refer to a nucleotide, oligonucleotide,
25 polynucleotide, or any fragment thereof. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material.

"Operably linked" refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with a second nucleic acid sequence. For instance, a promoter is operably
30 linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Operably linked DNA sequences may be in close proximity or contiguous and, where necessary to join two protein coding regions, in the same reading frame.

"Peptide nucleic acid" (PNA) refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of

amino acid residues ending in lysine. The terminal lysine confers solubility to the composition. PNAs preferentially bind complementary single stranded DNA or RNA and stop transcript elongation, and may be pegylated to extend their lifespan in the cell.

“Post-translational modification” of an PKIN may involve lipidation, glycosylation, phosphorylation, acetylation, racemization, proteolytic cleavage, and other modifications known in the art. These processes may occur synthetically or biochemically. Biochemical modifications will vary by cell type depending on the enzymatic milieu of PKIN.

“Probe” refers to nucleic acid sequences encoding PKIN, their complements, or fragments thereof, which are used to detect identical, allelic or related nucleic acid sequences. Probes are isolated oligonucleotides or polynucleotides attached to a detectable label or reporter molecule. Typical labels include radioactive isotopes, ligands, chemiluminescent agents, and enzymes. “Primers” are short nucleic acids, usually DNA oligonucleotides, which may be annealed to a target polynucleotide by complementary base-pairing. The primer may then be extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification (and identification) of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR).

Probes and primers as used in the present invention typically comprise at least 15 contiguous nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also be employed, such as probes and primers that comprise at least 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers may be considerably longer than these examples, and it is understood that any length supported by the specification, including the tables, figures, and Sequence Listing, may be used.

Methods for preparing and using probes and primers are described in the references, for example Sambrook, J. et al. (1989) Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; Ausubel, F.M. et al. (1987) Current Protocols in Molecular Biology, Greene Publ. Assoc. & Wiley-Intersciences, New York NY; Innis, M. et al. (1990) PCR Protocols, A Guide to Methods and Applications, Academic Press, San Diego CA. PCR primer pairs can be derived from a known sequence, for example, by using computer programs intended for that purpose such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge MA).

Oligonucleotides for use as primers are selected using software known in the art for such purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to 100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to 5,000 nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer selection programs have incorporated additional features for expanded capabilities. For example, the PrimOU

primer selection program (available to the public from the Genome Center at University of Texas South West Medical Center, Dallas TX) is capable of choosing specific primers from megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3 primer selection program (available to the public from the Whitehead Institute/MIT Center for Genome Research, Cambridge MA) allows the user to input a “mispriming library,” in which sequences to avoid as primer binding sites are user-specified. Primer3 is useful, in particular, for the selection of oligonucleotides for microarrays. (The source code for the latter two primer selection programs may also be obtained from their respective sources and modified to meet the user’s specific needs.) The PrimeGen program (available to the public from the UK Human Genome Mapping Project Resource Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing selection of primers that hybridize to either the most conserved or least conserved regions of aligned nucleic acid sequences. Hence, this program is useful for identification of both unique and conserved oligonucleotides and polynucleotide fragments. The oligonucleotides and polynucleotide fragments identified by any of the above selection methods are useful in hybridization technologies, for example, as PCR or sequencing primers, microarray elements, or specific probes to identify fully or partially complementary polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are not limited to those described above.

A “recombinant nucleic acid” is a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two or more otherwise separated segments of sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques such as those described in Sambrook, *supra*. The term recombinant includes nucleic acids that have been altered solely by addition, substitution, or deletion of a portion of the nucleic acid. Frequently, a recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence. Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

Alternatively, such recombinant nucleic acids may be part of a viral vector, e.g., based on a vaccinia virus, that could be used to vaccinate a mammal wherein the recombinant nucleic acid is expressed, inducing a protective immunological response in the mammal.

A “regulatory element” refers to a nucleic acid sequence usually derived from untranslated regions of a gene and includes enhancers, promoters, introns, and 5' and 3' untranslated regions (UTRs). Regulatory elements interact with host or viral proteins which control transcription, translation, or RNA stability.

“Reporter molecules” are chemical or biochemical moieties used for labeling a nucleic acid, amino acid, or antibody. Reporter molecules include radionuclides; enzymes; fluorescent,

chemiluminescent, or chromogenic agents; substrates; cofactors; inhibitors; magnetic particles; and other moieties known in the art.

An "RNA equivalent," in reference to a DNA sequence, is composed of the same linear sequence of nucleotides as the reference DNA sequence with the exception that all occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

The term "sample" is used in its broadest sense. A sample suspected of containing PKIN, nucleic acids encoding PKIN, or fragments thereof may comprise a bodily fluid; an extract from a cell, chromosome, organelle, or membrane isolated from a cell; a cell; genomic DNA, RNA, or cDNA, in solution or bound to a substrate; a tissue; a tissue print; etc.

The terms "specific binding" and "specifically binding" refer to that interaction between a protein or peptide and an agonist, an antibody, an antagonist, a small molecule, or any natural or synthetic binding composition. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide comprising the epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

The term "substantially purified" refers to nucleic acid or amino acid sequences that are removed from their natural environment and are isolated or separated, and are at least 60% free, preferably at least 75% free, and most preferably at least 90% free from other components with which they are naturally associated.

A "substitution" refers to the replacement of one or more amino acid residues or nucleotides by different amino acid residues or nucleotides, respectively.

"Substrate" refers to any suitable rigid or semi-rigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles and capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

A "transcript image" refers to the collective pattern of gene expression by a particular cell type or tissue under given conditions at a given time.

"Transformation" describes a process by which exogenous DNA is introduced into a recipient cell. Transformation may occur under natural or artificial conditions according to various methods well known in the art, and may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method for transformation is selected based on the type of host cell being transformed and may include, but is not limited to, bacteriophage or viral infection,

electroporation, heat shock, lipofection, and particle bombardment. The term "transformed cells" includes stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as transiently transformed cells which express the inserted DNA or RNA for limited periods of time.

5 A "transgenic organism," as used herein, is any organism, including but not limited to animals and plants, in which one or more of the cells of the organism contains heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with
10 a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or in vitro fertilization, but rather is directed to the introduction of a recombinant DNA molecule. The transgenic organisms contemplated in accordance with the present invention include bacteria, cyanobacteria, fungi, plants and animals. The isolated DNA of the present invention can be introduced into the host by methods known in the art, for example infection, transfection,
15 transformation or transconjugation. Techniques for transferring the DNA of the present invention into such organisms are widely known and provided in references such as Sambrook et al. (1989), supra.

 A "variant" of a particular nucleic acid sequence is defined as a nucleic acid sequence having at least 40% sequence identity to the particular nucleic acid sequence over a certain length of one of the
20 nucleic acid sequences using blastn with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of nucleic acids may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length. A variant may be described as, for example, an "allelic" (as
25 defined above), "splice," "species," or "polymorphic" variant. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternative splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or lack domains that are present in the reference molecule. Species variants are polynucleotide sequences that vary from one species to another. The resulting
30 polypeptides will generally have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one nucleotide base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

A "variant" of a particular polypeptide sequence is defined as a polypeptide sequence having at least 40% sequence identity to the particular polypeptide sequence over a certain length of one of the polypeptide sequences using blastp with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of polypeptides may show, for example, at least 50%, at least
 5 60%, at least 70%, at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length of one of the polypeptides.

THE INVENTION

10 The invention is based on the discovery of new human human kinases (PKIN), the polynucleotides encoding PKIN, and the use of these compositions for the diagnosis, treatment, or prevention of cancer, immune disorders, disorders affecting growth and development, cardiovascular diseases, and lipid disorders.

Table 1 summarizes the nomenclature for the full length polynucleotide and polypeptide
 15 sequences of the invention. Each polynucleotide and its corresponding polypeptide are correlated to a single Incyte project identification number (Incyte Project ID). Each polypeptide sequence is denoted by both a polypeptide sequence identification number (Polypeptide SEQ ID NO:) and an Incyte polypeptide sequence number (Incyte Polypeptide ID) as shown. Each polynucleotide sequence is denoted by both a polynucleotide sequence identification number (Polynucleotide SEQ ID NO:) and an
 20 Incyte polynucleotide consensus sequence number (Incyte Polynucleotide ID) as shown.

Table 2 shows sequences with homology to the polypeptides of the invention as identified by BLAST analysis against the GenBank protein (genpept) database. Columns 1 and 2 show the polypeptide sequence identification number (Polypeptide SEQ ID NO:) and the corresponding Incyte polypeptide sequence number (Incyte Polypeptide ID) for polypeptides of the invention. Column 3
 25 shows the GenBank identification number (Genbank ID NO:) of the nearest GenBank homolog. Column 4 shows the probability score for the match between each polypeptide and its GenBank homolog. Column 5 shows the annotation of the GenBank homolog along with relevant citations where applicable, all of which are expressly incorporated by reference herein.

Table 3 shows various structural features of the polypeptides of the invention. Columns 1 and 2
 30 show the polypeptide sequence identification number (SEQ ID NO:) and the corresponding Incyte polypeptide sequence number (Incyte Polypeptide ID) for each polypeptide of the invention. Column 3 shows the number of amino acid residues in each polypeptide. Column 4 shows potential phosphorylation sites, and column 5 shows potential glycosylation sites, as determined by the MOTIFS program of the GCG sequence analysis software package (Genetics Computer Group, Madison WI).

Column 6 shows amino acid residues comprising signature sequences, domains, and motifs. Column 7 shows analytical methods for protein structure/function analysis and in some cases, searchable databases to which the analytical methods were applied.

Together, Tables 2 and 3 summarize the properties of polypeptides of the invention, and these properties establish that the claimed polypeptides are human kinases. For example, SEQ ID NO:4 is 94% identical to rat serine/threonine kinase (GenBank ID g2052189) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is 0.0, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:4 also contains a protein kinase domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:4 is a protein kinase. In an alternate example, SEQ ID NO: 23 is 88% identical to murine protein kinase (GenBank ID g406058) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is 0.0, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:23 also contains an eukaryotic protein kinase domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:23 is a protein kinase. In an alternate example, SEQ ID NO:6 is 85% identical to rabbit myosin light chain kinase (GenBank ID g165506) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $1.5e-272$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:6 also contains a eukaryotic protein kinase domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from BLIMPS and MOTIFS analyses provide further corroborative evidence that SEQ ID NO:6 is a myosin light chain kinase. In an alternate example, SEQ ID NO:1 is 64% identical to murine serine/threonine kinase (GenBank ID g404634) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $4.5e-60$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:1 also contains a protein kinase domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from MOTIFS, BLIMPS and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:1 is a protein kinase, notably a serine/threonine kinase. In an alternate example, SEQ ID NO:19 is 49% identical to

human G-protein-coupled receptor kinase GRK4-beta (GenBank ID g992672) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $4.3e-129$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:19 also contains a regulator of G-protein signaling domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:19 is a G-protein-coupled receptor kinase. SEQ ID NO:2-3, SEQ ID NO:5, SEQ ID NO:7-18, SEQ ID NO:20-22 and SEQ ID NO:24-26 were analyzed and annotated in a similar manner. The algorithms and parameters for the analysis of SEQ ID NO:1-26 are described in Table 7.

As shown in Table 4, the full length polynucleotide sequences of the present invention were assembled using cDNA sequences or coding (exon) sequences derived from genomic DNA, or any combination of these two types of sequences. Columns 1 and 2 list the polynucleotide sequence identification number (Polynucleotide SEQ ID NO:) and the corresponding Incyte polynucleotide consensus sequence number (Incyte Polynucleotide ID) for each polynucleotide of the invention. Column 3 shows the length of each polynucleotide sequence in basepairs. Column 4 lists fragments of the polynucleotide sequences which are useful, for example, in hybridization or amplification technologies that identify SEQ ID NO:27-52 or that distinguish between SEQ ID NO:27-52 and related polynucleotide sequences. Column 5 shows identification numbers corresponding to cDNA sequences, coding sequences (exons) predicted from genomic DNA, and/or sequence assemblages comprised of both cDNA and genomic DNA. These sequences were used to assemble the full length polynucleotide sequences of the invention. Columns 6 and 7 of Table 4 show the nucleotide start (5') and stop (3') positions of the cDNA and/or genomic sequences in column 5 relative to their respective full length sequences.

The identification numbers in Column 5 of Table 4 may refer specifically, for example, to Incyte cDNAs along with their corresponding cDNA libraries. For example, 6829315H1 is the identification number of an Incyte cDNA sequence, and SINTNOR01 is the cDNA library from which it is derived. Incyte cDNAs for which cDNA libraries are not indicated were derived from pooled cDNA libraries (e.g., 55057226H1). Alternatively, the identification numbers in column 5 may refer to GenBank cDNAs or ESTs (e.g., g2954208) which contributed to the assembly of the full length polynucleotide sequences. In addition, the identification numbers in column 5 may identify sequences derived from the ENSEMBL (The Sanger Centre, Cambridge, UK) database (*i.e.*, those sequences including the designation "ENST"). Alternatively, the identification numbers in column 5 may be derived from the NCBI RefSeq Nucleotide Sequence Records Database (*i.e.*, those sequences including

the designation “NM” or “NT”) or the NCBI RefSeq Protein Sequence Records (*i.e.*, those sequences including the designation “NP”). Alternatively, the identification numbers in column 5 may refer to assemblages of both cDNA and Genscan-predicted exons brought together by an “exon stitching” algorithm. For example, FL_XXXXXX_ N_1 _ N_2 YYYYY_ N_3 _ N_4 represents a “stitched” sequence in which XXXXXX is the identification number of the cluster of sequences to which the algorithm was applied, and YYYYY is the number of the prediction generated by the algorithm, and $N_{1,2,3,...}$, if present, represent specific exons that may have been manually edited during analysis (See Example V).

Alternatively, the identification numbers in column 5 may refer to assemblages of exons brought together by an “exon-stretching” algorithm. For example, FLXXXXXX_gAAAAA_gBBBBB_1_N is the identification number of a “stretched” sequence, with XXXXXX being the Incyte project identification number, gAAAAA being the GenBank identification number of the human genomic sequence to which the “exon-stretching” algorithm was applied, gBBBBB being the GenBank identification number or NCBI RefSeq identification number of the nearest GenBank protein homolog, and N referring to specific exons (See Example V). In instances where a RefSeq sequence was used as a protein homolog for the “exon-stretching” algorithm, a RefSeq identifier (denoted by “NM,” “NP,” or “NT”) may be used in place of the GenBank identifier (*i.e.*, gBBBBB).

Alternatively, a prefix identifies component sequences that were hand-edited, predicted from genomic DNA sequences, or derived from a combination of sequence analysis methods. The following Table lists examples of component sequence prefixes and corresponding sequence analysis methods associated with the prefixes (see Example IV and Example V).

Prefix	Type of analysis and/or examples of programs
GNN, GFG, ENST	Exon prediction from genomic sequences using, for example, GENSCAN (Stanford University, CA, USA) or FGENES (Computer Genomics Group, The Sanger Centre, Cambridge, UK).
GBI	Hand-edited analysis of genomic sequences.
FL	Stitched or stretched genomic sequences (see Example V).

In some cases, Incyte cDNA coverage redundant with the sequence coverage shown in column 5 was obtained to confirm the final consensus polynucleotide sequence, but the relevant Incyte cDNA identification numbers are not shown.

Table 5 shows the representative cDNA libraries for those full length polynucleotide sequences which were assembled using Incyte cDNA sequences. The representative cDNA library is the Incyte cDNA library which is most frequently represented by the Incyte cDNA sequences which were used to

assemble and confirm the above polynucleotide sequences. The tissues and vectors which were used to construct the cDNA libraries shown in Table 5 are described in Table 6.

The invention also encompasses PKIN variants. A preferred PKIN variant is one which has at least about 80%, or alternatively at least about 90%, or even at least about 95% amino acid sequence identity to the PKIN amino acid sequence, and which contains at least one functional or structural characteristic of PKIN.

The invention also encompasses polynucleotides which encode PKIN. In a particular embodiment, the invention encompasses a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:27-52, which encodes PKIN. The polynucleotide sequences of SEQ ID NO:27-52, as presented in the Sequence Listing, embrace the equivalent RNA sequences, wherein occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

The invention also encompasses a variant of a polynucleotide sequence encoding PKIN. In particular, such a variant polynucleotide sequence will have at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to the polynucleotide sequence encoding PKIN. A particular aspect of the invention encompasses a variant of a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:27-52 which has at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:27-52. Any one of the polynucleotide variants described above can encode an amino acid sequence which contains at least one functional or structural characteristic of PKIN.

It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of polynucleotide sequences encoding PKIN, some bearing minimal similarity to the polynucleotide sequences of any known and naturally occurring gene, may be produced. Thus, the invention contemplates each and every possible variation of polynucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the polynucleotide sequence of naturally occurring PKIN, and all such variations are to be considered as being specifically disclosed.

Although nucleotide sequences which encode PKIN and its variants are generally capable of hybridizing to the nucleotide sequence of the naturally occurring PKIN under appropriately selected conditions of stringency, it may be advantageous to produce nucleotide sequences encoding PKIN or its derivatives possessing a substantially different codon usage, e.g., inclusion of non-naturally occurring codons. Codons may be selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons

are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding PKIN and its derivatives without altering the encoded amino acid sequences include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

5 The invention also encompasses production of DNA sequences which encode PKIN and PKIN derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding PKIN or any fragment thereof.

10 Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed polynucleotide sequences, and, in particular, to those shown in SEQ ID NO:27-52 and fragments thereof under various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.* 152:507-511.) Hybridization conditions, including annealing and wash conditions, are described in
15 “Definitions.”

 Methods for DNA sequencing are well known in the art and may be used to practice any of the embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE (US Biochemical, Cleveland OH), Taq polymerase (Applied Biosystems), thermostable T7 polymerase (Amersham Pharmacia Biotech, Piscataway NJ), or
20 combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies, Gaithersburg MD). Preferably, sequence preparation is automated with machines such as the MICROLAB 2200 liquid transfer system (Hamilton, Reno NV), PTC200 thermal cycler (MJ Research, Watertown MA) and ABI CATALYST 800 thermal cycler (Applied Biosystems). Sequencing is then carried out using either the ABI 373 or 377 DNA sequencing
25 system (Applied Biosystems), the MEGABACE 1000 DNA sequencing system (Molecular Dynamics, Sunnyvale CA), or other systems known in the art. The resulting sequences are analyzed using a variety of algorithms which are well known in the art. (See, e.g., Ausubel, F.M. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY, unit 7.7; Meyers, R.A. (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853.)

30 The nucleic acid sequences encoding PKIN may be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences, such as promoters and regulatory elements. For example, one method which may be employed, restriction-site PCR, uses universal and nested primers to amplify unknown sequence from genomic DNA within a cloning vector. (See, e.g., Sarkar, G. (1993) *PCR Methods Applic.* 2:318-322.)

Another method, inverse PCR, uses primers that extend in divergent directions to amplify unknown sequence from a circularized template. The template is derived from restriction fragments comprising a known genomic locus and surrounding sequences. (See, e.g., Triglia, T. et al. (1988) *Nucleic Acids Res.* 16:8186.) A third method, capture PCR, involves PCR amplification of DNA fragments adjacent to known sequences in human and yeast artificial chromosome DNA. (See, e.g., Lagerstrom, M. et al. (1991) *PCR Methods Applic.* 1:111-119.) In this method, multiple restriction enzyme digestions and ligations may be used to insert an engineered double-stranded sequence into a region of unknown sequence before performing PCR. Other methods which may be used to retrieve unknown sequences are known in the art. (See, e.g., Parker, J.D. et al. (1991) *Nucleic Acids Res.* 19:3055-3060).

Additionally, one may use PCR, nested primers, and PROMOTERFINDER libraries (Clontech, Palo Alto CA) to walk genomic DNA. This procedure avoids the need to screen libraries and is useful in finding intron/exon junctions. For all PCR-based methods, primers may be designed using commercially available software, such as OLIGO 4.06 primer analysis software (National Biosciences, Plymouth MN) or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the template at temperatures of about 68°C to 72°C.

When screening for full length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. In addition, random-primed libraries, which often include sequences containing the 5' regions of genes, are preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into 5' non-transcribed regulatory regions.

Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different nucleotide-specific, laser-stimulated fluorescent dyes, and a charge coupled device camera for detection of the emitted wavelengths. Output/light intensity may be converted to electrical signal using appropriate software (e.g., GENOTYPER and SEQUENCE NAVIGATOR, Applied Biosystems), and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for sequencing small DNA fragments which may be present in limited amounts in a particular sample.

In another embodiment of the invention, polynucleotide sequences or fragments thereof which encode PKIN may be cloned in recombinant DNA molecules that direct expression of PKIN, or fragments or functional equivalents thereof, in appropriate host cells. Due to the inherent degeneracy of

the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be produced and used to express PKIN.

The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter PKIN-encoding sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-mediated site-directed mutagenesis may be used to introduce mutations that create new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

The nucleotides of the present invention may be subjected to DNA shuffling techniques such as MOLECULARBREEDING (Maxygen Inc., Santa Clara CA; described in U.S. Patent Number 5,837,458; Chang, C.-C. et al. (1999) Nat. Biotechnol. 17:793-797; Christians, F.C. et al. (1999) Nat. Biotechnol. 17:259-264; and Crameri, A. et al. (1996) Nat. Biotechnol. 14:315-319) to alter or improve the biological properties of PKIN, such as its biological or enzymatic activity or its ability to bind to other molecules or compounds. DNA shuffling is a process by which a library of gene variants is produced using PCR-mediated recombination of gene fragments. The library is then subjected to selection or screening procedures that identify those gene variants with the desired properties. These preferred variants may then be pooled and further subjected to recursive rounds of DNA shuffling and selection/screening. Thus, genetic diversity is created through "artificial" breeding and rapid molecular evolution. For example, fragments of a single gene containing random point mutations may be recombined, screened, and then reshuffled until the desired properties are optimized. Alternatively, fragments of a given gene may be recombined with fragments of homologous genes in the same gene family, either from the same or different species, thereby maximizing the genetic diversity of multiple naturally occurring genes in a directed and controllable manner.

In another embodiment, sequences encoding PKIN may be synthesized, in whole or in part, using chemical methods well known in the art. (See, e.g., Caruthers, M.H. et al. (1980) Nucleic Acids Symp. Ser. 7:215-223; and Horn, T. et al. (1980) Nucleic Acids Symp. Ser. 7:225-232.) Alternatively, PKIN itself or a fragment thereof may be synthesized using chemical methods. For example, peptide synthesis can be performed using various solution-phase or solid-phase techniques. (See, e.g., Creighton, T. (1984) Proteins, Structures and Molecular Properties, WH Freeman, New York NY, pp. 55-60; and Roberge, J.Y. et al. (1995) Science 269:202-204.) Automated synthesis may be achieved using the ABI 431A peptide synthesizer (Applied Biosystems). Additionally, the amino acid sequence of PKIN, or any part thereof, may be altered during direct synthesis and/or combined with sequences

from other proteins, or any part thereof, to produce a variant polypeptide or a polypeptide having a sequence of a naturally occurring polypeptide.

The peptide may be substantially purified by preparative high performance liquid chromatography. (See, e.g., Chiez, R.M. and F.Z. Regnier (1990) *Methods Enzymol.* 182:392-421.)

5 The composition of the synthetic peptides may be confirmed by amino acid analysis or by sequencing. (See, e.g., Creighton, supra, pp. 28-53.)

In order to express a biologically active PKIN, the nucleotide sequences encoding PKIN or derivatives thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a
10 suitable host. These elements include regulatory sequences, such as enhancers, constitutive and inducible promoters, and 5' and 3' untranslated regions in the vector and in polynucleotide sequences encoding PKIN. Such elements may vary in their strength and specificity. Specific initiation signals may also be used to achieve more efficient translation of sequences encoding PKIN. Such signals include the ATG initiation codon and adjacent sequences, e.g. the Kozak sequence. In cases where
15 sequences encoding PKIN and its initiation codon and upstream regulatory sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including an in-frame ATG initiation codon should be provided by the vector. Exogenous translational elements and initiation codons may be of various origins, both natural
20 and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate for the particular host cell system used. (See, e.g., Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162.)

Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding PKIN and appropriate transcriptional and translational control
25 elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. (See, e.g., Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY, ch. 4, 8, and 16-17; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, ch. 9, 13, and 16.)

A variety of expression vector/host systems may be utilized to contain and express sequences
30 encoding PKIN. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or

animal cell systems. (See, e.g., Sambrook, supra; Ausubel, supra; Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509; Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945; Takamatsu, N. (1987) EMBO J. 6:307-311; The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196; Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659; and Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355.) Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. (See, e.g., Di Nicola, M. et al. (1998) Cancer Gen. Ther. 5(6):350-356; Yu, M. et al. (1993) Proc. Natl. Acad. Sci. USA 90(13):6340-6344; Buller, R.M. et al. (1985) Nature 317(6040):813-815; McGregor, D.P. et al. (1994) Mol. Immunol. 31(3):219-226; and Verma, I.M. and N. Somia (1997) Nature 389:239-242.) The invention is not limited by the host cell employed.

In bacterial systems, a number of cloning and expression vectors may be selected depending upon the use intended for polynucleotide sequences encoding PKIN. For example, routine cloning, subcloning, and propagation of polynucleotide sequences encoding PKIN can be achieved using a multifunctional *E. coli* vector such as PBLUESCRIPT (Stratagene, La Jolla CA) or PSPORT1 plasmid (Life Technologies). Ligation of sequences encoding PKIN into the vector's multiple cloning site disrupts the *lacZ* gene, allowing a colorimetric screening procedure for identification of transformed bacteria containing recombinant molecules. In addition, these vectors may be useful for in vitro transcription, dideoxy sequencing, single strand rescue with helper phage, and creation of nested deletions in the cloned sequence. (See, e.g., Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509.) When large quantities of PKIN are needed, e.g. for the production of antibodies, vectors which direct high level expression of PKIN may be used. For example, vectors containing the strong, inducible SP6 or T7 bacteriophage promoter may be used.

Yeast expression systems may be used for production of PKIN. A number of vectors containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGH promoters, may be used in the yeast *Saccharomyces cerevisiae* or *Pichia pastoris*. In addition, such vectors direct either the secretion or intracellular retention of expressed proteins and enable integration of foreign sequences into the host genome for stable propagation. (See, e.g., Ausubel, 1995, supra; Bitter, G.A. et al. (1987) Methods Enzymol. 153:516-544; and Scorer, C.A. et al. (1994) Bio/Technology 12:181-184.)

Plant systems may also be used for expression of PKIN. Transcription of sequences encoding PKIN may be driven by viral promoters, e.g., the 35S and 19S promoters of CaMV used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) EMBO J. 6:307-311).

Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used. (See, e.g., Coruzzi, G. et al. (1984) EMBO J. 3:1671-1680; Broglie, R. et al. (1984) Science 224:838-843; and Winter, J. et al. (1991) Results Probl. Cell Differ. 17:85-105.) These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. (See, e.g., The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196.)

In mammalian cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, sequences encoding PKIN may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain infective virus which expresses PKIN in host cells. (See, e.g., Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659.) In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells. SV40 or EBV-based vectors may also be used for high-level protein expression.

Human artificial chromosomes (HACs) may also be employed to deliver larger fragments of DNA than can be contained in and expressed from a plasmid. HACs of about 6 kb to 10 Mb are constructed and delivered via conventional delivery methods (liposomes, polycationic amino polymers, or vesicles) for therapeutic purposes. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355.)

For long term production of recombinant proteins in mammalian systems, stable expression of PKIN in cell lines is preferred. For example, sequences encoding PKIN can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for about 1 to 2 days in enriched media before being switched to selective media. The purpose of the selectable marker is to confer resistance to a selective agent, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be propagated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase and adenine phosphoribosyltransferase genes, for use in *tk⁻* and *apr⁻* cells, respectively. (See, e.g., Wigler, M. et al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.) Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to methotrexate; *neo* confers resistance to the aminoglycosides neomycin and G-418; and *als* and *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively. (See, e.g., Wigler, M. et al. (1980)

Proc. Natl. Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14.) Additional selectable genes have been described, e.g., *trpB* and *hisD*, which alter cellular requirements for metabolites. (See, e.g., Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. USA 85:8047-8051.) Visible markers, e.g., anthocyanins, green fluorescent proteins (GFP; Clontech), β glucuronidase and its substrate β -glucuronide, or luciferase and its substrate luciferin may be used. These markers can be used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system. (See, e.g., Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, the presence and expression of the gene may need to be confirmed. For example, if the sequence encoding PKIN is inserted within a marker gene sequence, transformed cells containing sequences encoding PKIN can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding PKIN under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

In general, host cells that contain the nucleic acid sequence encoding PKIN and that express PKIN may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations, PCR amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein sequences.

Immunological methods for detecting and measuring the expression of PKIN using either specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on PKIN is preferred, but a competitive binding assay may be employed. These and other assays are well known in the art. (See, e.g., Hampton, R. et al. (1990) Serological Methods, a Laboratory Manual, APS Press, St. Paul MN, Sect. IV; Coligan, J.E. et al. (1997) Current Protocols in Immunology, Greene Pub. Associates and Wiley-Interscience, New York NY; and Pound, J.D. (1998) Immunochemical Protocols, Humana Press, Totowa NJ.)

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding PKIN include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, the sequences encoding PKIN, or any fragments thereof, may be cloned into a vector for the production of

an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits, such as those provided by Amersham Pharmacia Biotech, Promega (Madison WI), and US
5 Biochemical. Suitable reporter molecules or labels which may be used for ease of detection include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with nucleotide sequences encoding PKIN may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein
10 produced by a transformed cell may be secreted or retained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode PKIN may be designed to contain signal sequences which direct secretion of PKIN through a prokaryotic or eukaryotic cell membrane.

In addition, a host cell strain may be chosen for its ability to modulate expression of the
15 inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" or "pro" form of the protein may also be used to specify protein targeting, folding, and/or activity. Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities
20 (e.g., CHO, HeLa, MDCK, HEK293, and WI38) are available from the American Type Culture Collection (ATCC, Manassas VA) and may be chosen to ensure the correct modification and processing of the foreign protein.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding PKIN may be ligated to a heterologous sequence resulting in translation of a fusion
25 protein in any of the aforementioned host systems. For example, a chimeric PKIN protein containing a heterologous moiety that can be recognized by a commercially available antibody may facilitate the screening of peptide libraries for inhibitors of PKIN activity. Heterologous protein and peptide moieties may also facilitate purification of fusion proteins using commercially available affinity matrices. Such moieties include, but are not limited to, glutathione S-transferase (GST), maltose binding protein
30 (MBP), thioredoxin (Trx), calmodulin binding peptide (CBP), 6-His, FLAG, *c-myc*, and hemagglutinin (HA). GST, MBP, Trx, CBP, and 6-His enable purification of their cognate fusion proteins on immobilized glutathione, maltose, phenylarsine oxide, calmodulin, and metal-chelate resins, respectively. FLAG, *c-myc*, and hemagglutinin (HA) enable immunoaffinity purification of fusion proteins using commercially available monoclonal and polyclonal antibodies that specifically recognize

these epitope tags. A fusion protein may also be engineered to contain a proteolytic cleavage site located between the PKIN encoding sequence and the heterologous protein sequence, so that PKIN may be cleaved away from the heterologous moiety following purification. Methods for fusion protein expression and purification are discussed in Ausubel (1995, supra, ch. 10). A variety of commercially available kits may also be used to facilitate expression and purification of fusion proteins.

In a further embodiment of the invention, synthesis of radiolabeled PKIN may be achieved in vitro using the TNT rabbit reticulocyte lysate or wheat germ extract system (Promega). These systems couple transcription and translation of protein-coding sequences operably associated with the T7, T3, or SP6 promoters. Translation takes place in the presence of a radiolabeled amino acid precursor, for example, ³⁵S-methionine.

PKIN of the present invention or fragments thereof may be used to screen for compounds that specifically bind to PKIN. At least one and up to a plurality of test compounds may be screened for specific binding to PKIN. Examples of test compounds include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

In one embodiment, the compound thus identified is closely related to the natural ligand of PKIN, e.g., a ligand or fragment thereof, a natural substrate, a structural or functional mimetic, or a natural binding partner. (See, e.g., Coligan, J.E. et al. (1991) Current Protocols in Immunology 1(2): Chapter 5.) Similarly, the compound can be closely related to the natural receptor to which PKIN binds, or to at least a fragment of the receptor, e.g., the ligand binding site. In either case, the compound can be rationally designed using known techniques. In one embodiment, screening for these compounds involves producing appropriate cells which express PKIN, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or E. coli. Cells expressing PKIN or cell membrane fractions which contain PKIN are then contacted with a test compound and binding, stimulation, or inhibition of activity of either PKIN or the compound is analyzed.

An assay may simply test binding of a test compound to the polypeptide, wherein binding is detected by a fluorophore, radioisotope, enzyme conjugate, or other detectable label. For example, the assay may comprise the steps of combining at least one test compound with PKIN, either in solution or affixed to a solid support, and detecting the binding of PKIN to the compound.

Alternatively, the assay may detect or measure binding of a test compound in the presence of a labeled competitor. Additionally, the assay may be carried out using cell-free preparations, chemical libraries, or natural product mixtures, and the test compound(s) may be free in solution or affixed to a solid support.

PKIN of the present invention or fragments thereof may be used to screen for compounds that modulate the activity of PKIN. Such compounds may include agonists, antagonists, or partial or

inverse agonists. In one embodiment, an assay is performed under conditions permissive for PKIN activity, wherein PKIN is combined with at least one test compound, and the activity of PKIN in the presence of a test compound is compared with the activity of PKIN in the absence of the test compound. A change in the activity of PKIN in the presence of the test compound is indicative of a compound that modulates the activity of PKIN. Alternatively, a test compound is combined with an in vitro or cell-free system comprising PKIN under conditions suitable for PKIN activity, and the assay is performed. In either of these assays, a test compound which modulates the activity of PKIN may do so indirectly and need not come in direct contact with the test compound. At least one and up to a plurality of test compounds may be screened.

In another embodiment, polynucleotides encoding PKIN or their mammalian homologs may be “knocked out” in an animal model system using homologous recombination in embryonic stem (ES) cells. Such techniques are well known in the art and are useful for the generation of animal models of human disease. (See, e.g., U.S. Patent Number 5,175,383 and U.S. Patent Number 5,767,337.) For example, mouse ES cells, such as the mouse 129/SvJ cell line, are derived from the early mouse embryo and grown in culture. The ES cells are transformed with a vector containing the gene of interest disrupted by a marker gene, e.g., the neomycin phosphotransferase gene (neo; Capecchi, M.R. (1989) Science 244:1288-1292). The vector integrates into the corresponding region of the host genome by homologous recombination. Alternatively, homologous recombination takes place using the Cre-loxP system to knockout a gene of interest in a tissue- or developmental stage-specific manner (Marth, J.D. (1996) Clin. Invest. 97:1999-2002; Wagner, K.U. et al. (1997) Nucleic Acids Res. 25:4323-4330). Transformed ES cells are identified and microinjected into mouse cell blastocysts such as those from the C57BL/6 mouse strain. The blastocysts are surgically transferred to pseudopregnant dams, and the resulting chimeric progeny are genotyped and bred to produce heterozygous or homozygous strains. Transgenic animals thus generated may be tested with potential therapeutic or toxic agents.

Polynucleotides encoding PKIN may also be manipulated in vitro in ES cells derived from human blastocysts. Human ES cells have the potential to differentiate into at least eight separate cell lineages including endoderm, mesoderm, and ectodermal cell types. These cell lineages differentiate into, for example, neural cells, hematopoietic lineages, and cardiomyocytes (Thomson, J.A. et al. (1998) Science 282:1145-1147).

Polynucleotides encoding PKIN can also be used to create “knockin” humanized animals (pigs) or transgenic animals (mice or rats) to model human disease. With knockin technology, a region of a polynucleotide encoding PKIN is injected into animal ES cells, and the injected sequence integrates into the animal cell genome. Transformed cells are injected into blastulae, and the blastulae are implanted as described above. Transgenic progeny or inbred lines are studied and treated with potential

pharmaceutical agents to obtain information on treatment of a human disease. Alternatively, a mammal inbred to overexpress PKIN, e.g., by secreting PKIN in its milk, may also serve as a convenient source of that protein (Janne, J. et al. (1998) *Biotechnol. Annu. Rev.* 4:55-74).

THERAPEUTICS

5 Chemical and structural similarity, e.g., in the context of sequences and motifs, exists between regions of PKIN and human kinases. In addition, the expression of PKIN is closely associated with lipid disorders, pancreatic islet cells, liver disease, leukocytes, umbilical endothelial cells, cancer, as well as, normal and diseased brain, renal, reproductive, bladder tumor, posterior hippocampus, kidney, small intestine, colon, and digestive tissues. Therefore, PKIN appears to play a
10 role in cancer, immune disorders, disorders affecting growth and development, cardiovascular diseases, and lipid disorders. In the treatment of disorders associated with increased PKIN expression or activity, it is desirable to decrease the expression or activity of PKIN. In the treatment of disorders associated with decreased PKIN expression or activity, it is desirable to increase the expression or activity of PKIN.

15 Therefore, in one embodiment, PKIN or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of PKIN. Examples of such disorders include, but are not limited to, a cancer, such as adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal
20 tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus, leukemias such as multiple myeloma and lymphomas such as Hodgkin's disease; an immune disorder, such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune
25 polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or
30 pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; a growth and developmental

disorder, such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of

5 the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus, renal tubular acidosis, anemia, Cushing's syndrome, achondroplastic dwarfism, Duchenne and Becker muscular dystrophy, epilepsy, gonadal dysgenesis, WAGR syndrome (Wilms' tumor, aniridia, genitourinary abnormalities, and

10 mental retardation), Smith-Magenis syndrome, myelodysplastic syndrome, hereditary mucoepithelial dysplasia, hereditary keratodermas, hereditary neuropathies such as Charcot-Marie-Tooth disease and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders such as Sydenham's chorea and cerebral palsy, spina bifida, anencephaly, craniorachischisis, congenital glaucoma, cataract, and sensorineural hearing loss; a cardiovascular disease, such as arteriovenous fistula, atherosclerosis,

15 hypertension, vasculitis, Raynaud's disease, aneurysms, arterial dissections, varicose veins, thrombophlebitis and phlebothrombosis, vascular tumors, and complications of thrombolysis, balloon angioplasty, vascular replacement, and coronary artery bypass graft surgery, congestive heart failure, ischemic heart disease, angina pectoris, myocardial infarction, hypertensive heart disease, degenerative valvular heart disease, calcific aortic valve stenosis, congenitally bicuspid aortic valve, mitral annular calcification, mitral valve prolapse, rheumatic fever and rheumatic heart disease, infective endocarditis,

20 nonbacterial thrombotic endocarditis, endocarditis of systemic lupus erythematosus, carcinoid heart disease, cardiomyopathy, myocarditis, pericarditis, neoplastic heart disease, congenital heart disease, and complications of cardiac transplantation, congenital lung anomalies, atelectasis, pulmonary congestion and edema, pulmonary embolism, pulmonary hemorrhage, pulmonary infarction, pulmonary

25 hypertension, vascular sclerosis, obstructive pulmonary disease, restrictive pulmonary disease, chronic obstructive pulmonary disease, emphysema, chronic bronchitis, bronchial asthma, bronchiectasis, bacterial pneumonia, viral and mycoplasmal pneumonia, lung abscess, pulmonary tuberculosis, diffuse interstitial diseases, pneumoconioses, sarcoidosis, idiopathic pulmonary fibrosis, desquamative interstitial pneumonitis, hypersensitivity pneumonitis, pulmonary eosinophilia bronchiolitis

30 obliterans-organizing pneumonia, diffuse pulmonary hemorrhage syndromes, Goodpasture's syndromes, idiopathic pulmonary hemosiderosis, pulmonary involvement in collagen-vascular disorders, pulmonary alveolar proteinosis, lung tumors, inflammatory and noninflammatory pleural effusions, pneumothorax, pleural tumors, drug-induced lung disease, radiation-induced lung disease, and complications of lung transplantation; and a lipid disorder, such as fatty liver, cholestasis, primary biliary cirrhosis, carnitine

deficiency, carnitine palmitoyltransferase deficiency, myoadenylate deaminase deficiency, hypertriglyceridemia, lipid storage disorders such as Fabry's disease, Gaucher's disease, Niemann-Pick's disease, metachromatic leukodystrophy, adrenoleukodystrophy, GM₂ gangliosidosis, and ceroid lipofuscinosis, abetalipoproteinemia, Tangier disease, hyperlipoproteinemia, diabetes mellitus, 5 lipodystrophy, lipomatosis, acute panniculitis, disseminated fat necrosis, adiposis dolorosa, lipoid adrenal hyperplasia, minimal change disease, lipomas, atherosclerosis, hypercholesterolemia, hypercholesterolemia with hypertriglyceridemia, primary hypoalphalipoproteinemia, hypothyroidism, renal disease, liver disease, lecithin:cholesterol acyltransferase deficiency, cerebrotendinous xanthomatosis, sitosterolemia, hypocholesterolemia, Tay-Sachs disease, Sandhoff's disease, 10 hyperlipidemia, hyperlipemia, lipid myopathies, and obesity.

In another embodiment, a vector capable of expressing PKIN or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of PKIN including, but not limited to, those described above.

In a further embodiment, a composition comprising a substantially purified PKIN in 15 conjunction with a suitable pharmaceutical carrier may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of PKIN including, but not limited to, those provided above.

In still another embodiment, an agonist which modulates the activity of PKIN may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity 20 of PKIN including, but not limited to, those listed above.

In a further embodiment, an antagonist of PKIN may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of PKIN. Examples of such disorders include, but are not limited to, those cancer, immune disorders, disorders affecting growth and development, cardiovascular diseases, and lipid disorders described above. In one aspect, an antibody 25 which specifically binds PKIN may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissues which express PKIN.

In an additional embodiment, a vector expressing the complement of the polynucleotide encoding PKIN may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of PKIN including, but not limited to, those described above.

30 In other embodiments, any of the proteins, antagonists, antibodies, agonists, complementary sequences, or vectors of the invention may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various

disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

An antagonist of PKIN may be produced using methods which are generally known in the art. In particular, purified PKIN may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind PKIN. Antibodies to PKIN may also be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. Neutralizing antibodies (i.e., those which inhibit dimer formation) are generally preferred for therapeutic use.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, humans, and others may be immunized by injection with PKIN or with any fragment or oligopeptide thereof which has immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, KLH, and dinitrophenol. Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and Corynebacterium parvum are especially preferable.

It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to PKIN have an amino acid sequence consisting of at least about 5 amino acids, and generally will consist of at least about 10 amino acids. It is also preferable that these oligopeptides, peptides, or fragments are identical to a portion of the amino acid sequence of the natural protein. Short stretches of PKIN amino acids may be fused with those of another protein, such as KLH, and antibodies to the chimeric molecule may be produced.

Monoclonal antibodies to PKIN may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique. (See, e.g., Kohler, G. et al. (1975) Nature 256:495-497; Kozbor, D. et al. (1985) J. Immunol. Methods 81:31-42; Cote, R.J. et al. (1983) Proc. Natl. Acad. Sci. USA 80:2026-2030; and Cole, S.P. et al. (1984) Mol. Cell Biol. 62:109-120.)

In addition, techniques developed for the production of "chimeric antibodies," such as the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity, can be used. (See, e.g., Morrison, S.L. et al. (1984) Proc. Natl. Acad. Sci. USA 81:6851-6855; Neuberger, M.S. et al. (1984) Nature 312:604-608; and Takeda, S. et al. (1985) Nature 314:452-454.) Alternatively, techniques described for the production of single chain antibodies may be adapted, using methods known in the art, to produce PKIN-specific single

chain antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be generated by chain shuffling from random combinatorial immunoglobulin libraries. (See, e.g., Burton, D.R. (1991) Proc. Natl. Acad. Sci. USA 88:10134-10137.)

Antibodies may also be produced by inducing in vivo production in the lymphocyte population
5 or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature. (See, e.g., Orlandi, R. et al. (1989) Proc. Natl. Acad. Sci. USA 86:3833-3837; Winter, G. et al. (1991) Nature 349:293-299.)

Antibody fragments which contain specific binding sites for PKIN may also be generated. For example, such fragments include, but are not limited to, F(ab')₂ fragments produced by pepsin digestion
10 of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity. (See, e.g., Huse, W.D. et al. (1989) Science 246:1275-1281.)

Various immunoassays may be used for screening to identify antibodies having the desired
15 specificity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between PKIN and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering PKIN epitopes is generally used, but a competitive binding assay may also be employed
20 (Pound, supra).

Various methods such as Scatchard analysis in conjunction with radioimmunoassay techniques may be used to assess the affinity of antibodies for PKIN. Affinity is expressed as an association constant, K_a , which is defined as the molar concentration of PKIN-antibody complex divided by the molar concentrations of free antigen and free antibody under equilibrium conditions. The K_a determined
25 for a preparation of polyclonal antibodies, which are heterogeneous in their affinities for multiple PKIN epitopes, represents the average affinity, or avidity, of the antibodies for PKIN. The K_a determined for a preparation of monoclonal antibodies, which are monospecific for a particular PKIN epitope, represents a true measure of affinity. High-affinity antibody preparations with K_a ranging from about 10^9 to 10^{12} L/mole are preferred for use in immunoassays in which the PKIN-antibody complex must
30 withstand rigorous manipulations. Low-affinity antibody preparations with K_a ranging from about 10^6 to 10^7 L/mole are preferred for use in immunopurification and similar procedures which ultimately require dissociation of PKIN, preferably in active form, from the antibody (Catty, D. (1988) Antibodies, Volume I: A Practical Approach, IRL Press, Washington DC; Liddell, J.E. and A. Cryer (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons, New York NY).

The titer and avidity of polyclonal antibody preparations may be further evaluated to determine the quality and suitability of such preparations for certain downstream applications. For example, a polyclonal antibody preparation containing at least 1-2 mg specific antibody/ml, preferably 5-10 mg specific antibody/ml, is generally employed in procedures requiring precipitation of PKIN-antibody complexes. Procedures for evaluating antibody specificity, titer, and avidity, and guidelines for antibody quality and usage in various applications, are generally available. (See, e.g., Catty, supra, and Coligan et al. supra.)

In another embodiment of the invention, the polynucleotides encoding PKIN, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, modifications of gene expression can be achieved by designing complementary sequences or antisense molecules (DNA, RNA, PNA, or modified oligonucleotides) to the coding or regulatory regions of the gene encoding PKIN. Such technology is well known in the art, and antisense oligonucleotides or larger fragments can be designed from various locations along the coding or control regions of sequences encoding PKIN. (See, e.g., Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press Inc., Totawa NJ.)

In therapeutic use, any gene delivery system suitable for introduction of the antisense sequences into appropriate target cells can be used. Antisense sequences can be delivered intracellularly in the form of an expression plasmid which, upon transcription, produces a sequence complementary to at least a portion of the cellular sequence encoding the target protein. (See, e.g., Slater, J.E. et al. (1998) *J. Allergy Clin. Immunol.* 102(3):469-475; and Scanlon, K.J. et al. (1995) 9(13):1288-1296.) Antisense sequences can also be introduced intracellularly through the use of viral vectors, such as retrovirus and adeno-associated virus vectors. (See, e.g., Miller, A.D. (1990) *Blood* 76:271; Ausubel, supra; Uckert, W. and W. Walther (1994) *Pharmacol. Ther.* 63(3):323-347.) Other gene delivery mechanisms include liposome-derived systems, artificial viral envelopes, and other systems known in the art. (See, e.g., Rossi, J.J. (1995) *Br. Med. Bull.* 51(1):217-225; Boado, R.J. et al. (1998) *J. Pharm. Sci.* 87(11):1308-1315; and Morris, M.C. et al. (1997) *Nucleic Acids Res.* 25(14):2730-2736.)

In another embodiment of the invention, polynucleotides encoding PKIN may be used for somatic or germline gene therapy. Gene therapy may be performed to (i) correct a genetic deficiency (e.g., in the cases of severe combined immunodeficiency (SCID)-X1 disease characterized by X-linked inheritance (Cavazzana-Calvo, M. et al. (2000) *Science* 288:669-672), severe combined immunodeficiency syndrome associated with an inherited adenosine deaminase (ADA) deficiency (Blaese, R.M. et al. (1995) *Science* 270:475-480; Bordignon, C. et al. (1995) *Science* 270:470-475), cystic fibrosis (Zabner, J. et al. (1993) *Cell* 75:207-216; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:643-666; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:667-703), thalassemias, familial

hypercholesterolemia, and hemophilia resulting from Factor VIII or Factor IX deficiencies (Crystal, R.G. (1995) Science 270:404-410; Verma, I.M. and N. Somia (1997) Nature 389:239-242)), (ii) express a conditionally lethal gene product (e.g., in the case of cancers which result from unregulated cell proliferation), or (iii) express a protein which affords protection against intracellular parasites (e.g., against human retroviruses, such as human immunodeficiency virus (HIV) (Baltimore, D. (1988) Nature 335:395-396; Poeschla, E. et al. (1996) Proc. Natl. Acad. Sci. USA. 93:11395-11399), hepatitis B or C virus (HBV, HCV); fungal parasites, such as Candida albicans and Paracoccidioides brasiliensis; and protozoan parasites such as Plasmodium falciparum and Trypanosoma cruzi). In the case where a genetic deficiency in PKIN expression or regulation causes disease, the expression of PKIN from an appropriate population of transduced cells may alleviate the clinical manifestations caused by the genetic deficiency.

In a further embodiment of the invention, diseases or disorders caused by deficiencies in PKIN are treated by constructing mammalian expression vectors encoding PKIN and introducing these vectors by mechanical means into PKIN-deficient cells. Mechanical transfer technologies for use with cells in vivo or ex vitro include (i) direct DNA microinjection into individual cells, (ii) ballistic gold particle delivery, (iii) liposome-mediated transfection, (iv) receptor-mediated gene transfer, and (v) the use of DNA transposons (Morgan, R.A. and W.F. Anderson (1993) Annu. Rev. Biochem. 62:191-217; Ivics, Z. (1997) Cell 91:501-510; Boulay, J-L. and H. Récipon (1998) Curr. Opin. Biotechnol. 9:445-450).

Expression vectors that may be effective for the expression of PKIN include, but are not limited to, the pCDNA 3.1, EPITAG, PRCCMV2, PREP, PVAX vectors (Invitrogen, Carlsbad CA), PCMV-SCRIPT, PCMV-TAG, PEGSH/PERV (Stratagene, La Jolla CA), and PTET-OFF, PTET-ON, PTRE2, PTRE2-LUC, PTK-HYG (Clontech, Palo Alto CA). PKIN may be expressed using (i) a constitutively active promoter, (e.g., from cytomegalovirus (CMV), Rous sarcoma virus (RSV), SV40 virus, thymidine kinase (TK), or β -actin genes), (ii) an inducible promoter (e.g., the tetracycline-regulated promoter (Gossen, M. and H. Bujard (1992) Proc. Natl. Acad. Sci. USA 89:5547-5551; Gossen, M. et al. (1995) Science 268:1766-1769; Rossi, F.M.V. and H.M. Blau (1998) Curr. Opin. Biotechnol. 9:451-456), commercially available in the T-REX plasmid (Invitrogen)); the ecdysone-inducible promoter (available in the plasmids PVGRXR and PIND; Invitrogen); the FK506/rapamycin inducible promoter; or the RU486/mifepristone inducible promoter (Rossi, F.M.V. and Blau, H.M. supra)), or (iii) a tissue-specific promoter or the native promoter of the endogenous gene encoding PKIN from a normal individual.

Commercially available liposome transformation kits (e.g., the PERFECT LIPID TRANSFECTION KIT, available from Invitrogen) allow one with ordinary skill in the art to deliver polynucleotides to target cells in culture and require minimal effort to optimize experimental

parameters. In the alternative, transformation is performed using the calcium phosphate method (Graham, F.L. and A.J. Eb (1973) *Virology* 52:456-467), or by electroporation (Neumann, E. et al. (1982) *EMBO J.* 1:841-845). The introduction of DNA to primary cells requires modification of these standardized mammalian transfection protocols.

5 In another embodiment of the invention, diseases or disorders caused by genetic defects with respect to PKIN expression are treated by constructing a retrovirus vector consisting of (i) the polynucleotide encoding PKIN under the control of an independent promoter or the retrovirus long terminal repeat (LTR) promoter, (ii) appropriate RNA packaging signals, and (iii) a Rev-responsive element (RRE) along with additional retrovirus *cis*-acting RNA sequences and coding sequences
10 required for efficient vector propagation. Retrovirus vectors (e.g., PFB and PFBNEO) are commercially available (Stratagene) and are based on published data (Riviere, I. et al. (1995) *Proc. Natl. Acad. Sci. USA* 92:6733-6737), incorporated by reference herein. The vector is propagated in an appropriate vector producing cell line (VPCL) that expresses an envelope gene with a tropism for receptors on the target cells or a promiscuous envelope protein such as VSVg (Armentano, D. et al.
15 (1987) *J. Virol.* 61:1647-1650; Bender, M.A. et al. (1987) *J. Virol.* 61:1639-1646; Adam, M.A. and A.D. Miller (1988) *J. Virol.* 62:3802-3806; Dull, T. et al. (1998) *J. Virol.* 72:8463-8471; Zufferey, R. et al. (1998) *J. Virol.* 72:9873-9880). U.S. Patent Number 5,910,434 to Rigg ("Method for obtaining retrovirus packaging cell lines producing high transducing efficiency retroviral supernatant") discloses a method for obtaining retrovirus packaging cell lines and is hereby incorporated by reference.

20 Propagation of retrovirus vectors, transduction of a population of cells (e.g., CD4⁺ T-cells), and the return of transduced cells to a patient are procedures well known to persons skilled in the art of gene therapy and have been well documented (Ranga, U. et al. (1997) *J. Virol.* 71:7020-7029; Bauer, G. et al. (1997) *Blood* 89:2259-2267; Bonyhadi, M.L. (1997) *J. Virol.* 71:4707-4716; Ranga, U. et al. (1998) *Proc. Natl. Acad. Sci. USA* 95:1201-1206; Su, L. (1997) *Blood* 89:2283-2290).

25 In the alternative, an adenovirus-based gene therapy delivery system is used to deliver polynucleotides encoding PKIN to cells which have one or more genetic abnormalities with respect to the expression of PKIN. The construction and packaging of adenovirus-based vectors are well known to those with ordinary skill in the art. Replication defective adenovirus vectors have proven to be versatile for importing genes encoding immunoregulatory proteins into intact islets in the pancreas
30 (Csete, M.E. et al. (1995) *Transplantation* 27:263-268). Potentially useful adenoviral vectors are described in U.S. Patent Number 5,707,618 to Armentano ("Adenovirus vectors for gene therapy"), hereby incorporated by reference. For adenoviral vectors, see also Antinozzi, P.A. et al. (1999) *Annu. Rev. Nutr.* 19:511-544 and Verma, I.M. and N. Somia (1997) *Nature* 18:389:239-242, both incorporated by reference herein.

In another alternative, a herpes-based, gene therapy delivery system is used to deliver polynucleotides encoding PKIN to target cells which have one or more genetic abnormalities with respect to the expression of PKIN. The use of herpes simplex virus (HSV)-based vectors may be especially valuable for introducing PKIN to cells of the central nervous system, for which HSV has a tropism. The construction and packaging of herpes-based vectors are well known to those with ordinary skill in the art. A replication-competent herpes simplex virus (HSV) type 1-based vector has been used to deliver a reporter gene to the eyes of primates (Liu, X. et al. (1999) *Exp. Eye Res.* 169:385-395). The construction of a HSV-1 virus vector has also been disclosed in detail in U.S. Patent Number 5,804,413 to DeLuca ("Herpes simplex virus strains for gene transfer"), which is hereby incorporated by reference. U.S. Patent Number 5,804,413 teaches the use of recombinant HSV d92 which consists of a genome containing at least one exogenous gene to be transferred to a cell under the control of the appropriate promoter for purposes including human gene therapy. Also taught by this patent are the construction and use of recombinant HSV strains deleted for ICP4, ICP27 and ICP22. For HSV vectors, see also Goins, W.F. et al. (1999) *J. Virol.* 73:519-532 and Xu, H. et al. (1994) *Dev. Biol.* 163:152-161, hereby incorporated by reference. The manipulation of cloned herpesvirus sequences, the generation of recombinant virus following the transfection of multiple plasmids containing different segments of the large herpesvirus genomes, the growth and propagation of herpesvirus, and the infection of cells with herpesvirus are techniques well known to those of ordinary skill in the art.

In another alternative, an alphavirus (positive, single-stranded RNA virus) vector is used to deliver polynucleotides encoding PKIN to target cells. The biology of the prototypic alphavirus, Semliki Forest Virus (SFV), has been studied extensively and gene transfer vectors have been based on the SFV genome (Garoff, H. and K.-J. Li (1998) *Curr. Opin. Biotechnol.* 9:464-469). During alphavirus RNA replication, a subgenomic RNA is generated that normally encodes the viral capsid proteins. This subgenomic RNA replicates to higher levels than the full length genomic RNA, resulting in the overproduction of capsid proteins relative to the viral proteins with enzymatic activity (e.g., protease and polymerase). Similarly, inserting the coding sequence for PKIN into the alphavirus genome in place of the capsid-coding region results in the production of a large number of PKIN-coding RNAs and the synthesis of high levels of PKIN in vector transduced cells. While alphavirus infection is typically associated with cell lysis within a few days, the ability to establish a persistent infection in hamster normal kidney cells (BHK-21) with a variant of Sindbis virus (SIN) indicates that the lytic replication of alphaviruses can be altered to suit the needs of the gene therapy application (Dryga, S.A. et al. (1997) *Virology* 228:74-83). The wide host range of alphaviruses will allow the introduction of PKIN into a variety of cell types. The specific transduction of a subset of cells in a population may

require the sorting of cells prior to transduction. The methods of manipulating infectious cDNA clones of alphaviruses, performing alphavirus cDNA and RNA transfections, and performing alphavirus infections, are well known to those with ordinary skill in the art.

Oligonucleotides derived from the transcription initiation site, e.g., between about positions -10 and +10 from the start site, may also be employed to inhibit gene expression. Similarly, inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature. (See, e.g., Gee, J.E. et al. (1994) in Huber, B.E. and B.I. Carr, Molecular and Immunologic Approaches, Futura Publishing, Mt. Kisco NY, pp. 163-177.) A complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. For example, engineered hammerhead motif ribozyme molecules may specifically and efficiently catalyze endonucleolytic cleavage of sequences encoding PKIN.

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites, including the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides, corresponding to the region of the target gene containing the cleavage site, may be evaluated for secondary structural features which may render the oligonucleotide inoperable. The suitability of candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

Complementary ribonucleic acid molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding PKIN. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesize complementary RNA, constitutively or inducibly, can be introduced into cell lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages

within the backbone of the molecule. This concept is inherent in the production of PNAs and can be extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

5 An additional embodiment of the invention encompasses a method for screening for a compound which is effective in altering expression of a polynucleotide encoding PKIN. Compounds which may be effective in altering expression of a specific polynucleotide may include, but are not limited to, oligonucleotides, antisense oligonucleotides, triple helix-forming oligonucleotides, transcription factors and other polypeptide transcriptional regulators, and non-macromolecular
10 chemical entities which are capable of interacting with specific polynucleotide sequences. Effective compounds may alter polynucleotide expression by acting as either inhibitors or promoters of polynucleotide expression. Thus, in the treatment of disorders associated with increased PKIN expression or activity, a compound which specifically inhibits expression of the polynucleotide encoding PKIN may be therapeutically useful, and in the treatment of disorders associated with
15 decreased PKIN expression or activity, a compound which specifically promotes expression of the polynucleotide encoding PKIN may be therapeutically useful.

At least one, and up to a plurality, of test compounds may be screened for effectiveness in altering expression of a specific polynucleotide. A test compound may be obtained by any method commonly known in the art, including chemical modification of a compound known to be effective in
20 altering polynucleotide expression; selection from an existing, commercially-available or proprietary library of naturally-occurring or non-natural chemical compounds; rational design of a compound based on chemical and/or structural properties of the target polynucleotide; and selection from a library of chemical compounds created combinatorially or randomly. A sample comprising a polynucleotide encoding PKIN is exposed to at least one test compound thus obtained. The sample
25 may comprise, for example, an intact or permeabilized cell, or an *in vitro* cell-free or reconstituted biochemical system. Alterations in the expression of a polynucleotide encoding PKIN are assayed by any method commonly known in the art. Typically, the expression of a specific nucleotide is detected by hybridization with a probe having a nucleotide sequence complementary to the sequence of the polynucleotide encoding PKIN. The amount of hybridization may be quantified, thus forming the
30 basis for a comparison of the expression of the polynucleotide both with and without exposure to one or more test compounds. Detection of a change in the expression of a polynucleotide exposed to a test compound indicates that the test compound is effective in altering the expression of the polynucleotide. A screen for a compound effective in altering expression of a specific polynucleotide can be carried out, for example, using a *Schizosaccharomyces pombe* gene expression system (Atkins,
35 D. et al. (1999) U.S. Patent No. 5,932,435; Arndt, G.M. et al. (2000) Nucleic Acids Res. 28:E15) or a

human cell line such as HeLa cell (Clarke, M.L. et al. (2000) Biochem. Biophys. Res. Commun. 268:8-13). A particular embodiment of the present invention involves screening a combinatorial library of oligonucleotides (such as deoxyribonucleotides, ribonucleotides, peptide nucleic acids, and modified oligonucleotides) for antisense activity against a specific polynucleotide sequence (Bruce, T.W. et al. (1997) U.S. Patent No. 5,686,242; Bruce, T.W. et al. (2000) U.S. Patent No. 6,022,691).

Many methods for introducing vectors into cells or tissues are available and equally suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers may be achieved using methods which are well known in the art. (See, e.g., Goldman, C.K. et al. (1997) Nat. Biotechnol. 15:462-466.)

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as humans, dogs, cats, cows, horses, rabbits, and monkeys.

An additional embodiment of the invention relates to the administration of a composition which generally comprises an active ingredient formulated with a pharmaceutically acceptable excipient. Excipients may include, for example, sugars, starches, celluloses, gums, and proteins. Various formulations are commonly known and are thoroughly discussed in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing, Easton PA). Such compositions may consist of PKIN, antibodies to PKIN, and mimetics, agonists, antagonists, or inhibitors of PKIN.

The compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, pulmonary, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

Compositions for pulmonary administration may be prepared in liquid or dry powder form. These compositions are generally aerosolized immediately prior to inhalation by the patient. In the case of small molecules (e.g. traditional low molecular weight organic drugs), aerosol delivery of fast-acting formulations is well-known in the art. In the case of macromolecules (e.g. larger peptides and proteins), recent developments in the field of pulmonary delivery via the alveolar region of the lung have enabled the practical delivery of drugs such as insulin to blood circulation (see, e.g., Patton, J.S. et al., U.S. Patent No. 5,997,848). Pulmonary delivery has the advantage of administration without needle injection, and obviates the need for potentially toxic penetration enhancers.

Compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art.

Specialized forms of compositions may be prepared for direct intracellular delivery of macromolecules comprising PKIN or fragments thereof. For example, liposome preparations containing a cell-impermeable macromolecule may promote cell fusion and intracellular delivery of the macromolecule. Alternatively, PKIN or a fragment thereof may be joined to a short cationic N-terminal portion from the HIV Tat-1 protein. Fusion proteins thus generated have been found to transduce into the cells of all tissues, including the brain, in a mouse model system (Schwarze, S.R. et al. (1999) Science 285:1569-1572).

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells, or in animal models such as mice, rats, rabbits, dogs, monkeys, or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of active ingredient, for example PKIN or fragments thereof, antibodies of PKIN, and agonists, antagonists or inhibitors of PKIN, which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or with experimental animals, such as by calculating the ED_{50} (the dose therapeutically effective in 50% of the population) or LD_{50} (the dose lethal to 50% of the population) statistics. The dose ratio of toxic to therapeutic effects is the therapeutic index, which can be expressed as the LD_{50}/ED_{50} ratio. Compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used to formulate a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that includes the ED_{50} with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, the sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy. Long-acting compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from about 0.1 μg to 100,000 μg , up to a total dose of about 1 gram, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their
5 inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

DIAGNOSTICS

In another embodiment, antibodies which specifically bind PKIN may be used for the diagnosis of disorders characterized by expression of PKIN, or in assays to monitor patients being treated with
10 PKIN or agonists, antagonists, or inhibitors of PKIN. Antibodies useful for diagnostic purposes may be prepared in the same manner as described above for therapeutics. Diagnostic assays for PKIN include methods which utilize the antibody and a label to detect PKIN in human body fluids or in extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled by covalent or non-covalent attachment of a reporter molecule. A wide variety of reporter
15 molecules, several of which are described above, are known in the art and may be used.

A variety of protocols for measuring PKIN, including ELISAs, RIAs, and FACS, are known in the art and provide a basis for diagnosing altered or abnormal levels of PKIN expression. Normal or standard values for PKIN expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, for example, human subjects, with antibodies to PKIN under
20 conditions suitable for complex formation. The amount of standard complex formation may be quantitated by various methods, such as photometric means. Quantities of PKIN expressed in subject, control, and disease samples from biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides encoding PKIN may be used for
25 diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect and quantify gene expression in biopsied tissues in which expression of PKIN may be correlated with disease. The diagnostic assay may be used to determine absence, presence, and excess expression of PKIN, and to monitor regulation of PKIN levels during therapeutic intervention.

30 In one aspect, hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences, encoding PKIN or closely related molecules may be used to identify nucleic acid sequences which encode PKIN. The specificity of the probe, whether it is made from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification will determine whether the

probe identifies only naturally occurring sequences encoding PKIN, allelic variants, or related sequences.

Probes may also be used for the detection of related sequences, and may have at least 50% sequence identity to any of the PKIN encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and may be derived from the sequence of SEQ ID NO:27-52 or from genomic sequences including promoters, enhancers, and introns of the PKIN gene.

Means for producing specific hybridization probes for DNAs encoding PKIN include the cloning of polynucleotide sequences encoding PKIN or PKIN derivatives into vectors for the production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, by radionuclides such as ^{32}P or ^{35}S , or by enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

Polynucleotide sequences encoding PKIN may be used for the diagnosis of disorders associated with expression of PKIN. Examples of such disorders include, but are not limited to, a cancer, such as adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus, leukemias such as multiple myeloma and lymphomas such as Hodgkin's disease; an immune disorder, such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; a growth and developmental disorder, such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease

(MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus, renal tubular acidosis, anemia, Cushing's syndrome, achondroplastic dwarfism, Duchenne and Becker muscular dystrophy, epilepsy, gonadal dysgenesis, WAGR syndrome (Wilms' tumor, aniridia, genitourinary abnormalities, and mental retardation), Smith-Magenis syndrome, myelodysplastic syndrome, hereditary mucoepithelial dysplasia, hereditary keratodermas, hereditary neuropathies such as Charcot-Marie-Tooth disease and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders such as Sydenham's chorea and cerebral palsy, spina bifida, anencephaly, craniorachischisis, congenital glaucoma, cataract, and sensorineural hearing loss; a cardiovascular disease, such as arteriovenous fistula, atherosclerosis, hypertension, vasculitis, Raynaud's disease, aneurysms, arterial dissections, varicose veins, thrombophlebitis and phlebothrombosis, vascular tumors, and complications of thrombolysis, balloon angioplasty, vascular replacement, and coronary artery bypass graft surgery, congestive heart failure, ischemic heart disease, angina pectoris, myocardial infarction, hypertensive heart disease, degenerative valvular heart disease, calcific aortic valve stenosis, congenitally bicuspid aortic valve, mitral annular calcification, mitral valve prolapse, rheumatic fever and rheumatic heart disease, infective endocarditis, nonbacterial thrombotic endocarditis, endocarditis of systemic lupus erythematosus, carcinoid heart disease, cardiomyopathy, myocarditis, pericarditis, neoplastic heart disease, congenital heart disease, and complications of cardiac transplantation, congenital lung anomalies, atelectasis, pulmonary congestion and edema, pulmonary embolism, pulmonary hemorrhage, pulmonary infarction, pulmonary hypertension, vascular sclerosis, obstructive pulmonary disease, restrictive pulmonary disease, chronic obstructive pulmonary disease, emphysema, chronic bronchitis, bronchial asthma, bronchiectasis, bacterial pneumonia, viral and mycoplasmal pneumonia, lung abscess, pulmonary tuberculosis, diffuse interstitial diseases, pneumoconioses, sarcoidosis, idiopathic pulmonary fibrosis, desquamative interstitial pneumonitis, hypersensitivity pneumonitis, pulmonary eosinophilia bronchiolitis obliterans-organizing pneumonia, diffuse pulmonary hemorrhage syndromes, Goodpasture's syndromes, idiopathic pulmonary hemosiderosis, pulmonary involvement in collagen-vascular disorders, pulmonary alveolar proteinosis, lung tumors, inflammatory and noninflammatory pleural effusions, pneumothorax, pleural tumors, drug-induced lung disease, radiation-induced lung disease, and complications of lung transplantation; and a lipid disorder, such as fatty liver, cholestasis, primary biliary cirrhosis, carnitine deficiency, carnitine palmitoyltransferase deficiency, myoadenylate deaminase deficiency,

hypertriglyceridemia, lipid storage disorders such Fabry's disease, Gaucher's disease, Niemann-Pick's disease, metachromatic leukodystrophy, adrenoleukodystrophy, GM₂ gangliosidosis, and ceroid lipofuscinosis, abetalipoproteinemia, Tangier disease, hyperlipoproteinemia, diabetes mellitus, lipodystrophy, lipomatoses, acute panniculitis, disseminated fat necrosis, adiposis dolorosa, lipid

5 adrenal hyperplasia, minimal change disease, lipomas, atherosclerosis, hypercholesterolemia, hypercholesterolemia with hypertriglyceridemia, primary hypoalphalipoproteinemia, hypothyroidism, renal disease, liver disease, lecithin:cholesterol acyltransferase deficiency, cerebrotendinous xanthomatosis, sitosterolemia, hypocholesterolemia, Tay-Sachs disease, Sandhoff's disease, hyperlipidemia, hyperlipemia, lipid myopathies, and obesity. The polynucleotide sequences encoding

10 PKIN may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; in dipstick, pin, and multiformat ELISA-like assays; and in microarrays utilizing fluids or tissues from patients to detect altered PKIN expression. Such qualitative or quantitative methods are well known in the art.

In a particular aspect, the nucleotide sequences encoding PKIN may be useful in assays that

15 detect the presence of associated disorders, particularly those mentioned above. The nucleotide sequences encoding PKIN may be labeled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantified and compared with a standard value. If the amount of signal in the patient sample is significantly altered in comparison to a control

20 sample then the presence of altered levels of nucleotide sequences encoding PKIN in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

In order to provide a basis for the diagnosis of a disorder associated with expression of PKIN, a

25 normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, encoding PKIN, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used.

30 Standard values obtained in this manner may be compared with values obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

Once the presence of a disorder is established and a treatment protocol is initiated, hybridization assays may be repeated on a regular basis to determine if the level of expression in the

patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

With respect to cancer, the presence of an abnormal amount of transcript (either under- or overexpressed) in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Additional diagnostic uses for oligonucleotides designed from the sequences encoding PKIN may involve the use of PCR. These oligomers may be chemically synthesized, generated enzymatically, or produced in vitro. Oligomers will preferably contain a fragment of a polynucleotide encoding PKIN, or a fragment of a polynucleotide complementary to the polynucleotide encoding PKIN, and will be employed under optimized conditions for identification of a specific gene or condition. Oligomers may also be employed under less stringent conditions for detection or quantification of closely related DNA or RNA sequences.

In a particular aspect, oligonucleotide primers derived from the polynucleotide sequences encoding PKIN may be used to detect single nucleotide polymorphisms (SNPs). SNPs are substitutions, insertions and deletions that are a frequent cause of inherited or acquired genetic disease in humans. Methods of SNP detection include, but are not limited to, single-stranded conformation polymorphism (SSCP) and fluorescent SSCP (fSSCP) methods. In SSCP, oligonucleotide primers derived from the polynucleotide sequences encoding PKIN are used to amplify DNA using the polymerase chain reaction (PCR). The DNA may be derived, for example, from diseased or normal tissue, biopsy samples, bodily fluids, and the like. SNPs in the DNA cause differences in the secondary and tertiary structures of PCR products in single-stranded form, and these differences are detectable using gel electrophoresis in non-denaturing gels. In fSSCP, the oligonucleotide primers are fluorescently labeled, which allows detection of the amplimers in high-throughput equipment such as DNA sequencing machines. Additionally, sequence database analysis methods, termed *in silico* SNP (isSNP), are capable of identifying polymorphisms by comparing the sequence of individual overlapping DNA fragments which assemble into a common consensus sequence. These computer-based methods filter out sequence variations due to laboratory preparation of DNA and sequencing errors using statistical models and automated analyses of DNA sequence chromatograms. In the alternative, SNPs may be detected and characterized by mass spectrometry using, for example, the high throughput MASSARRAY system (Sequenom, Inc., San Diego CA).

Methods which may also be used to quantify the expression of PKIN include radiolabeling or biotinylating nucleotides, coamplification of a control nucleic acid, and interpolating results from standard curves. (See, e.g., Melby, P.C. et al. (1993) J. Immunol. Methods 159:235-244; Duplaa, C. et al. (1993) Anal. Biochem. 212:229-236.) The speed of quantitation of multiple samples may be accelerated by running the assay in a high-throughput format where the oligomer or polynucleotide of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

In further embodiments, oligonucleotides or longer fragments derived from any of the polynucleotide sequences described herein may be used as elements on a microarray. The microarray can be used in transcript imaging techniques which monitor the relative expression levels of large numbers of genes simultaneously as described below. The microarray may also be used to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, to monitor progression/regression of disease as a function of gene expression, and to develop and monitor the activities of therapeutic agents in the treatment of disease. In particular, this information may be used to develop a pharmacogenomic profile of a patient in order to select the most appropriate and effective treatment regimen for that patient. For example, therapeutic agents which are highly effective and display the fewest side effects may be selected for a patient based on his/her pharmacogenomic profile.

In another embodiment, PKIN, fragments of PKIN, or antibodies specific for PKIN may be used as elements on a microarray. The microarray may be used to monitor or measure protein-protein interactions, drug-target interactions, and gene expression profiles, as described above.

A particular embodiment relates to the use of the polynucleotides of the present invention to generate a transcript image of a tissue or cell type. A transcript image represents the global pattern of gene expression by a particular tissue or cell type. Global gene expression patterns are analyzed by quantifying the number of expressed genes and their relative abundance under given conditions and at a given time. (See Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent Number 5,840,484, expressly incorporated by reference herein.) Thus a transcript image may be generated by hybridizing the polynucleotides of the present invention or their complements to the totality of transcripts or reverse transcripts of a particular tissue or cell type. In one embodiment, the hybridization takes place in high-throughput format, wherein the polynucleotides of the present invention or their complements comprise a subset of a plurality of elements on a microarray. The resultant transcript image would provide a profile of gene activity.

Transcript images may be generated using transcripts isolated from tissues, cell lines, biopsies, or other biological samples. The transcript image may thus reflect gene expression in vivo, as in the case of a tissue or biopsy sample, or in vitro, as in the case of a cell line.

Transcript images which profile the expression of the polynucleotides of the present invention
5 may also be used in conjunction with in vitro model systems and preclinical evaluation of
pharmaceuticals, as well as toxicological testing of industrial and naturally-occurring environmental
compounds. All compounds induce characteristic gene expression patterns, frequently termed
molecular fingerprints or toxicant signatures, which are indicative of mechanisms of action and toxicity
(Nuwaysir, E.F. et al. (1999) Mol. Carcinog. 24:153-159; Steiner, S. and N.L. Anderson (2000)
10 Toxicol. Lett. 112-113:467-471, expressly incorporated by reference herein). If a test compound has a
signature similar to that of a compound with known toxicity, it is likely to share those toxic properties.
These fingerprints or signatures are most useful and refined when they contain expression information
from a large number of genes and gene families. Ideally, a genome-wide measurement of expression
provides the highest quality signature. Even genes whose expression is not altered by any tested
15 compounds are important as well, as the levels of expression of these genes are used to normalize the
rest of the expression data. The normalization procedure is useful for comparison of expression data
after treatment with different compounds. While the assignment of gene function to elements of a
toxicant signature aids in interpretation of toxicity mechanisms, knowledge of gene function is not
necessary for the statistical matching of signatures which leads to prediction of toxicity. (See, for
20 example, Press Release 00-02 from the National Institute of Environmental Health Sciences, released
February 29, 2000, available at <http://www.niehs.nih.gov/oc/news/toxchip.htm>.) Therefore, it is
important and desirable in toxicological screening using toxicant signatures to include all expressed
gene sequences.

In one embodiment, the toxicity of a test compound is assessed by treating a biological sample
25 containing nucleic acids with the test compound. Nucleic acids that are expressed in the treated
biological sample are hybridized with one or more probes specific to the polynucleotides of the
present invention, so that transcript levels corresponding to the polynucleotides of the present
invention may be quantified. The transcript levels in the treated biological sample are compared with
levels in an untreated biological sample. Differences in the transcript levels between the two samples
30 are indicative of a toxic response caused by the test compound in the treated sample.

Another particular embodiment relates to the use of the polypeptide sequences of the present
invention to analyze the proteome of a tissue or cell type. The term proteome refers to the global
pattern of protein expression in a particular tissue or cell type. Each protein component of a proteome
can be subjected individually to further analysis. Proteome expression patterns, or profiles, are

analyzed by quantifying the number of expressed proteins and their relative abundance under given conditions and at a given time. A profile of a cell's proteome may thus be generated by separating and analyzing the polypeptides of a particular tissue or cell type. In one embodiment, the separation is achieved using two-dimensional gel electrophoresis, in which proteins from a sample are separated by isoelectric focusing in the first dimension, and then according to molecular weight by sodium dodecyl sulfate slab gel electrophoresis in the second dimension (Steiner and Anderson, *supra*). The proteins are visualized in the gel as discrete and uniquely positioned spots, typically by staining the gel with an agent such as Coomassie Blue or silver or fluorescent stains. The optical density of each protein spot is generally proportional to the level of the protein in the sample. The optical densities of equivalently positioned protein spots from different samples, for example, from biological samples either treated or untreated with a test compound or therapeutic agent, are compared to identify any changes in protein spot density related to the treatment. The proteins in the spots are partially sequenced using, for example, standard methods employing chemical or enzymatic cleavage followed by mass spectrometry. The identity of the protein in a spot may be determined by comparing its partial sequence, preferably of at least 5 contiguous amino acid residues, to the polypeptide sequences of the present invention. In some cases, further sequence data may be obtained for definitive protein identification.

A proteomic profile may also be generated using antibodies specific for PKIN to quantify the levels of PKIN expression. In one embodiment, the antibodies are used as elements on a microarray, and protein expression levels are quantified by exposing the microarray to the sample and detecting the levels of protein bound to each array element (Lueking, A. et al. (1999) *Anal. Biochem.* 270:103-111; Mendozze, L.G. et al. (1999) *Biotechniques* 27:778-788). Detection may be performed by a variety of methods known in the art, for example, by reacting the proteins in the sample with a thiol- or amino-reactive fluorescent compound and detecting the amount of fluorescence bound at each array element.

Toxicant signatures at the proteome level are also useful for toxicological screening, and should be analyzed in parallel with toxicant signatures at the transcript level. There is a poor correlation between transcript and protein abundances for some proteins in some tissues (Anderson, N.L. and J. Seilhamer (1997) *Electrophoresis* 18:533-537), so proteome toxicant signatures may be useful in the analysis of compounds which do not significantly affect the transcript image, but which alter the proteomic profile. In addition, the analysis of transcripts in body fluids is difficult, due to rapid degradation of mRNA, so proteomic profiling may be more reliable and informative in such cases.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins that are expressed in the treated biological sample are separated so that the amount of each protein can be quantified. The amount of each protein is compared to the amount of the corresponding protein in an untreated biological sample. A difference

in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample. Individual proteins are identified by sequencing the amino acid residues of the individual proteins and comparing these partial sequences to the polypeptides of the present invention.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins from the biological sample are incubated with antibodies specific to the polypeptides of the present invention. The amount of protein recognized by the antibodies is quantified. The amount of protein in the treated biological sample is compared with the amount in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci. USA 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. USA 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.) Various types of microarrays are well known and thoroughly described in DNA Microarrays: A Practical Approach, M. Schena, ed. (1999) Oxford University Press, London, hereby expressly incorporated by reference.

In another embodiment of the invention, nucleic acid sequences encoding PKIN may be used to generate hybridization probes useful in mapping the naturally occurring genomic sequence. Either coding or noncoding sequences may be used, and in some instances, noncoding sequences may be preferable over coding sequences. For example, conservation of a coding sequence among members of a multi-gene family may potentially cause undesired cross hybridization during chromosomal mapping. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.) Once mapped, the nucleic acid sequences of the invention may be used to develop genetic linkage maps, for example, which correlate the inheritance of a disease state with the inheritance of a particular chromosome region or restriction fragment length polymorphism (RFLP). (See, for example, Lander, E.S. and D. Botstein (1986) Proc. Natl. Acad. Sci. USA 83:7353-7357.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical and genetic map data. (See, e.g., Heinz-Ulrich, et al. (1995) in Meyers, supra, pp. 965-968.) Examples of genetic map data can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) World Wide Web site. Correlation between the location of the gene encoding PKIN on a physical map

and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder and thus may further positional cloning efforts.

In situ hybridization of chromosomal preparations and physical mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending genetic maps.

5 Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the exact chromosomal locus is not known. This information is valuable to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once the gene or genes responsible for a disease or syndrome have been crudely localized by genetic linkage to a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences
10 mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequence of the instant invention may also be used to detect differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier, or affected individuals.

In another embodiment of the invention, PKIN, its catalytic or immunogenic fragments, or
15 oligopeptides thereof can be used for screening libraries of compounds in any of a variety of drug screening techniques. The fragment employed in such screening may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. The formation of binding complexes between PKIN and the agent being tested may be measured.

Another technique for drug screening provides for high throughput screening of compounds
20 having suitable binding affinity to the protein of interest. (See, e.g., Geysen, et al. (1984) PCT application WO84/03564.) In this method, large numbers of different small test compounds are synthesized on a solid substrate. The test compounds are reacted with PKIN, or fragments thereof, and washed. Bound PKIN is then detected by methods well known in the art. Purified PKIN can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively,
25 non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding PKIN specifically compete with a test compound for binding PKIN. In this manner, antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PKIN.

30 In additional embodiments, the nucleotide sequences which encode PKIN may be used in any molecular biology techniques that have yet to be developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

5 The disclosures of all patents, applications and publications, mentioned above and below, including U.S. Ser. No. 60/212,073, U.S. Ser. No. 60/213,467, U.S. Ser. No. 60/215,651, U.S. Ser. No. 60/216,605, U.S. Ser. No. 60/218,372, and U.S. Ser. No. 60/228,056 are expressly incorporated by reference herein.

10 EXAMPLES

I. Construction of cDNA Libraries

Incyte cDNAs were derived from cDNA libraries described in the LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA) and shown in Table 4, column 5. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a
15 suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated from the lysates with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA
20 purity. In some cases, RNA was treated with DNase. For most libraries, poly(A)+ RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega), OLIGOTEX latex particles (QIAGEN, Chatsworth CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA purification kit (Ambion, Austin TX).

25 In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP vector system (Stratagene) or SUPERScript plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, supra, units 5.1-6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic
30 oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g.,

PBLUESCRIPT plasmid (Stratagene), PSPORT1 plasmid (Life Technologies), PCDNA2.1 plasmid (Invitrogen, Carlsbad CA), PBK-CMV plasmid (Stratagene), or pINCY (Incyte Genomics, Palo Alto CA), or derivatives thereof. Recombinant plasmids were transformed into competent *E. coli* cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 α , DH10B, or ElectroMAX DH10B from Life Technologies.

II. Isolation of cDNA Clones

Plasmids obtained as described in Example I were recovered from host cells by *in vivo* excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: a Magic or WIZARD Minipreps DNA purification system (Promega); an AGTC Miniprep purification kit (Edge Biosystems, Gaithersburg MD); and QIAWELL 8 Plasmid, QIAWELL 8 Plus Plasmid, QIAWELL 8 Ultra Plasmid purification systems or the R.E.A.L. PREP 96 plasmid purification kit from QIAGEN. Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format (Rao, V.B. (1994) Anal. Biochem. 216:1-14). Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Eugene OR) and a FLUOROSKAN II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

III. Sequencing and Analysis

Incyte cDNA recovered in plasmids as described in Example II were sequenced as follows. Sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 (Applied Biosystems) thermal cycler or the PTC-200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific) or the MICROLAB 2200 (Hamilton) liquid transfer system. cDNA sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems). Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics); the ABI PRISM 373 or 377 sequencing system (Applied Biosystems) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art. Reading frames within the cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997, *supra*, unit 7.7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example VIII.

The polynucleotide sequences derived from Incyte cDNAs were validated by removing vector, linker, and poly(A) sequences and by masking ambiguous bases, using algorithms and programs based on BLAST, dynamic programming, and dinucleotide nearest neighbor analysis. The Incyte cDNA sequences or translations thereof were then queried against a selection of public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases, and BLOCKS, PRINTS, DOMO, PRODOM, and hidden Markov model (HMM)-based protein family databases such as PFAM. (HMM is a probabilistic approach which analyzes consensus primary structures of gene families. See, for example, Eddy, S.R. (1996) *Curr. Opin. Struct. Biol.* 6:361-365.) The queries were performed using programs based on BLAST, FASTA, BLIMPS, and HMMER. The Incyte cDNA sequences were assembled to produce full length polynucleotide sequences. Alternatively, GenBank cDNAs, GenBank ESTs, stitched sequences, stretched sequences, or Genscan-predicted coding sequences (see Examples IV and V) were used to extend Incyte cDNA assemblages to full length. Assembly was performed using programs based on Phred, Phrap, and Consed, and cDNA assemblages were screened for open reading frames using programs based on GeneMark, BLAST, and FASTA. The full length polynucleotide sequences were translated to derive the corresponding full length polypeptide sequences. Alternatively, a polypeptide of the invention may begin at any of the methionine residues of the full length translated polypeptide. Full length polypeptide sequences were subsequently analyzed by querying against databases such as the GenBank protein databases (genpept), SwissProt, BLOCKS, PRINTS, DOMO, PRODOM, Prosite, and hidden Markov model (HMM)-based protein family databases such as PFAM. Full length polynucleotide sequences are also analyzed using MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Polynucleotide and polypeptide sequence alignments are generated using default parameters specified by the CLUSTAL algorithm as incorporated into the MEGALIGN multisequence alignment program (DNASTAR), which also calculates the percent identity between aligned sequences.

Table 7 summarizes the tools, programs, and algorithms used for the analysis and assembly of Incyte cDNA and full length sequences and provides applicable descriptions, references, and threshold parameters. The first column of Table 7 shows the tools, programs, and algorithms used, the second column provides brief descriptions thereof, the third column presents appropriate references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score or the lower the probability value, the greater the identity between two sequences).

The programs described above for the assembly and analysis of full length polynucleotide and polypeptide sequences were also used to identify polynucleotide sequence fragments from SEQ ID NO:27-52. Fragments from about 20 to about 4000 nucleotides which are useful in hybridization and amplification technologies are described in Table 4, column 4.

5 IV. Identification and Editing of Coding Sequences from Genomic DNA

Putative human kinases were initially identified by running the Genscan gene identification program against public genomic sequence databases (e.g., gbpri and gbhtg). Genscan is a general-purpose gene identification program which analyzes genomic DNA sequences from a variety of organisms (See Burge, C. and S. Karlin (1997) J. Mol. Biol. 268:78-94, and Burge, C. and S. Karlin 10 (1998) Curr. Opin. Struct. Biol. 8:346-354). The program concatenates predicted exons to form an assembled cDNA sequence extending from a methionine to a stop codon. The output of Genscan is a FASTA database of polynucleotide and polypeptide sequences. The maximum range of sequence for Genscan to analyze at once was set to 30 kb. To determine which of these Genscan predicted cDNA sequences encode human kinases, the encoded polypeptides were analyzed by querying against PFAM 15 models for human kinases. Potential human kinases were also identified by homology to Incyte cDNA sequences that had been annotated as human kinases. These selected Genscan-predicted sequences were then compared by BLAST analysis to the genpept and gbpri public databases. Where necessary, the Genscan-predicted sequences were then edited by comparison to the top BLAST hit from genpept to correct errors in the sequence predicted by Genscan, such as extra or omitted exons. BLAST analysis 20 was also used to find any Incyte cDNA or public cDNA coverage of the Genscan-predicted sequences, thus providing evidence for transcription. When Incyte cDNA coverage was available, this information was used to correct or confirm the Genscan predicted sequence. Full length polynucleotide sequences were obtained by assembling Genscan-predicted coding sequences with Incyte cDNA sequences and/or public cDNA sequences using the assembly process described in Example III. Alternatively, full length 25 polynucleotide sequences were derived entirely from edited or unedited Genscan-predicted coding sequences.

V. Assembly of Genomic Sequence Data with cDNA Sequence Data

"Stitched" Sequences

Partial cDNA sequences were extended with exons predicted by the Genscan gene identification 30 program described in Example IV. Partial cDNAs assembled as described in Example III were mapped to genomic DNA and parsed into clusters containing related cDNAs and Genscan exon predictions from one or more genomic sequences. Each cluster was analyzed using an algorithm based on graph theory and dynamic programming to integrate cDNA and genomic information, generating possible splice variants that were subsequently confirmed, edited, or extended to create a full length sequence.

Sequence intervals in which the entire length of the interval was present on more than one sequence in the cluster were identified, and intervals thus identified were considered to be equivalent by transitivity. For example, if an interval was present on a cDNA and two genomic sequences, then all three intervals were considered to be equivalent. This process allows unrelated but consecutive genomic sequences to be brought together, bridged by cDNA sequence. Intervals thus identified were then "stitched" together by the stitching algorithm in the order that they appear along their parent sequences to generate the longest possible sequence, as well as sequence variants. Linkages between intervals which proceed along one type of parent sequence (cDNA to cDNA or genomic sequence to genomic sequence) were given preference over linkages which change parent type (cDNA to genomic sequence). The resultant stitched sequences were translated and compared by BLAST analysis to the genpept and gbpri public databases. Incorrect exons predicted by Genscan were corrected by comparison to the top BLAST hit from genpept. Sequences were further extended with additional cDNA sequences, or by inspection of genomic DNA, when necessary.

"Stretched" Sequences

Partial DNA sequences were extended to full length with an algorithm based on BLAST analysis. First, partial cDNAs assembled as described in Example III were queried against public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases using the BLAST program. The nearest GenBank protein homolog was then compared by BLAST analysis to either Incyte cDNA sequences or GenScan exon predicted sequences described in Example IV. A chimeric protein was generated by using the resultant high-scoring segment pairs (HSPs) to map the translated sequences onto the GenBank protein homolog. Insertions or deletions may occur in the chimeric protein with respect to the original GenBank protein homolog. The GenBank protein homolog, the chimeric protein, or both were used as probes to search for homologous genomic sequences from the public human genome databases. Partial DNA sequences were therefore "stretched" or extended by the addition of homologous genomic sequences. The resultant stretched sequences were examined to determine whether it contained a complete gene.

VI. Chromosomal Mapping of PKIN Encoding Polynucleotides

The sequences which were used to assemble SEQ ID NO:27-52 were compared with sequences from the Incyte LIFESEQ database and public domain databases using BLAST and other implementations of the Smith-Waterman algorithm. Sequences from these databases that matched SEQ ID NO:27-52 were assembled into clusters of contiguous and overlapping sequences using assembly algorithms such as Phrap (Table 7). Radiation hybrid and genetic mapping data available from public resources such as the Stanford Human Genome Center (SHGC), Whitehead Institute for Genome Research (WIGR), and Généthon were used to determine if any of the clustered sequences

had been previously mapped. Inclusion of a mapped sequence in a cluster resulted in the assignment of all sequences of that cluster, including its particular SEQ ID NO:, to that map location.

Map locations are represented by ranges, or intervals, of human chromosomes. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Généthon which provide boundaries for radiation hybrid markers whose sequences were included in each of the clusters. Human genome maps and other resources available to the public, such as the NCBI "GeneMap'99" World Wide Web site (<http://www.ncbi.nlm.nih.gov/genemap/>), can be employed to determine if previously identified disease genes map within or in proximity to the intervals indicated above.

In this manner, SEQ ID NO:27 was mapped to chromosome 19 and SEQ ID NO:35 was mapped to chromosome 15 within the interval from 72.30 to 77.30 centiMorgans. SEQ ID NO:48 was mapped to chromosome 10 within the interval from 93.80 to 96.90 centiMorgans. SEQ ID NO:49 was mapped to chromosome 13 within the interval from 11.60 to 22.80 centiMorgans, to chromosome 17 within the interval from 0.60 to 14.80 centiMorgans, and to chromosome 20 within the interval from 57.70 to 64.10 centiMorgans. More than one map location is reported for SEQ ID NO:49, indicating that sequences having different map locations were assembled into a single cluster. This situation occurs, for example, when sequences having strong similarity, but not complete identity, are assembled into a single cluster.

VII. Analysis of Polynucleotide Expression

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, supra, ch. 7; Ausubel (1995) supra, ch. 4 and 16.)

Analogous computer techniques applying BLAST were used to search for identical or related molecules in cDNA databases such as GenBank or LIFESEQ (Incyte Genomics). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

$$\frac{\text{BLAST Score} \times \text{Percent Identity}}{5 \times \text{minimum} \{ \text{length}(\text{Seq. 1}), \text{length}(\text{Seq. 2}) \}}$$

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. The product score is a normalized value between 0 and 100, and is calculated as follows: the BLAST score is multiplied by the percent nucleotide identity and the product is divided by (5 times the length of the shorter of the two sequences). The BLAST score is calculated by assigning a score of +5 for every base that matches in a high-scoring segment pair (HSP), and -4 for every mismatch. Two sequences may share more than one HSP (separated by gaps). If there is more than one HSP, then the pair with the highest BLAST score is used to calculate the product score. The product score represents a balance between fractional overlap and quality in a BLAST alignment. For example, a product score of 100 is produced only for 100% identity over the entire length of the shorter of the two sequences being compared. A product score of 70 is produced either by 100% identity and 70% overlap at one end, or by 88% identity and 100% overlap at the other. A product score of 50 is produced either by 100% identity and 50% overlap at one end, or 79% identity and 100% overlap.

Alternatively, polynucleotide sequences encoding PKIN are analyzed with respect to the tissue sources from which they were derived. For example, some full length sequences are assembled, at least in part, with overlapping Incyte cDNA sequences (see Example III). Each cDNA sequence is derived from a cDNA library constructed from a human tissue. Each human tissue is classified into one of the following organ/tissue categories: cardiovascular system; connective tissue; digestive system; embryonic structures; endocrine system; exocrine glands; genitalia, female; genitalia, male; germ cells; hemic and immune system; liver; musculoskeletal system; nervous system; pancreas; respiratory system; sense organs; skin; stomatognathic system; unclassified/mixed; or urinary tract. The number of libraries in each category is counted and divided by the total number of libraries across all categories. Similarly, each human tissue is classified into one of the following disease/condition categories: cancer, cell line, developmental, inflammation, neurological, trauma, cardiovascular, pooled, and other, and the number of libraries in each category is counted and divided by the total number of libraries across all categories. The resulting percentages reflect the tissue- and disease-specific expression of cDNA encoding PKIN. cDNA sequences and cDNA library/tissue information are found in the LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA).

VIII. Extension of PKIN Encoding Polynucleotides

Full length polynucleotide sequences were also produced by extension of an appropriate fragment of the full length molecule using oligonucleotide primers designed from this fragment. One primer was synthesized to initiate 5' extension of the known fragment, and the other primer was

synthesized to initiate 3' extension of the known fragment. The initial primers were designed using OLIGO 4.06 software (National Biosciences), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations was avoided.

Selected human cDNA libraries were used to extend the sequence. If more than one extension was necessary or desired, additional or nested sets of primers were designed.

High fidelity amplification was obtained by PCR using methods well known in the art. PCR was performed in 96-well plates using the PTC-200 thermal cycler (MJ Research, Inc.). The reaction mix contained DNA template, 200 nmol of each primer, reaction buffer containing Mg^{2+} , $(NH_4)_2SO_4$, and 2-mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme (Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ were as follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well was determined by dispensing 100 μ l PICOGREEN quantitation reagent (0.25% (v/v) PICOGREEN; Molecular Probes, Eugene OR) dissolved in 1X TE and 0.5 μ l of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Costar, Acton MA), allowing the DNA to bind to the reagent. The plate was scanned in a Fluoroskan II (Labsystems Oy, Helsinki, Finland) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5 μ l to 10 μ l aliquot of the reaction mixture was analyzed by electrophoresis on a 1 % agarose gel to determine which reactions were successful in extending the sequence.

The extended nucleotides were desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For shotgun sequencing, the digested nucleotides were separated on low concentration (0.6 to 0.8%) agarose gels, fragments were excised, and agar digested with Agar ACE (Promega). Extended clones were religated using T4 ligase (New England Biolabs, Beverly MA) into pUC 18 vector (Amersham Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into competent *E. coli* cells. Transformed cells were selected on antibiotic-containing media, and individual colonies were picked and cultured overnight at 37°C in 384-well plates in LB/2x carb liquid media.

The cells were lysed, and DNA was amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA was quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries were reamplified using the same conditions as described above. Samples were diluted with 20% dimethylsulfoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems).

In like manner, full length polynucleotide sequences are verified using the above procedure or are used to obtain 5' regulatory sequences using the above procedure along with oligonucleotides designed for such extension, and an appropriate genomic library.

IX. Labeling and Use of Individual Hybridization Probes

Hybridization probes derived from SEQ ID NO:27-52 are employed to screen cDNAs, genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20 base pairs, is specifically described, essentially the same procedure is used with larger nucleotide fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 μ Ci of [γ -³²P] adenosine triphosphate (Amersham Pharmacia Biotech), and T4 polynucleotide kinase (DuPont NEN, Boston MA). The labeled oligonucleotides are substantially purified using a SEPHADEX G-25 superfine size exclusion dextran bead column (Amersham Pharmacia Biotech). An aliquot containing 10⁷ counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases: Ase I, Bgl II, Eco RI, Pst I, Xba I, or Pvu II (DuPont NEN).

The DNA from each digest is fractionated on a 0.7% agarose gel and transferred to nylon membranes (Nytran Plus, Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under conditions of up to, for example, 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate. Hybridization patterns are visualized using autoradiography or an alternative imaging means and compared.

X. Microarrays

The linkage or synthesis of array elements upon a microarray can be achieved utilizing photolithography, piezoelectric printing (ink-jet printing, See, e.g., Baldeschweiler, *supra.*), mechanical microspotting technologies, and derivatives thereof. The substrate in each of the aforementioned

technologies should be uniform and solid with a non-porous surface (Skena (1999), supra). Suggested substrates include silicon, silica, glass slides, glass chips, and silicon wafers. Alternatively, a procedure analogous to a dot or slot blot may also be used to arrange and link elements to the surface of a substrate using thermal, UV, chemical, or mechanical bonding procedures. A typical array may be produced using available methods and machines well known to those of ordinary skill in the art and may contain any appropriate number of elements. (See, e.g., Skena, M. et al. (1995) Science 270:467-470; Shalon, D. et al. (1996) Genome Res. 6:639-645; Marshall, A. and J. Hodgson (1998) Nat. Biotechnol. 16:27-31.)

Full length cDNAs, Expressed Sequence Tags (ESTs), or fragments or oligomers thereof may comprise the elements of the microarray. Fragments or oligomers suitable for hybridization can be selected using software well known in the art such as LASERGENE software (DNASTAR). The array elements are hybridized with polynucleotides in a biological sample. The polynucleotides in the biological sample are conjugated to a fluorescent label or other molecular tag for ease of detection. After hybridization, nonhybridized nucleotides from the biological sample are removed, and a fluorescence scanner is used to detect hybridization at each array element. Alternatively, laser desorption and mass spectrometry may be used for detection of hybridization. The degree of complementarity and the relative abundance of each polynucleotide which hybridizes to an element on the microarray may be assessed. In one embodiment, microarray preparation and usage is described in detail below.

Tissue or Cell Sample Preparation

Total RNA is isolated from tissue samples using the guanidinium thiocyanate method and poly(A)⁺ RNA is purified using the oligo-(dT) cellulose method. Each poly(A)⁺ RNA sample is reverse transcribed using MMLV reverse-transcriptase, 0.05 pg/μl oligo-(dT) primer (21mer), 1X first strand buffer, 0.03 units/μl RNase inhibitor, 500 μM dATP, 500 μM dGTP, 500 μM dTTP, 40 μM dCTP, 40 μM dCTP-Cy3 (BDS) or dCTP-Cy5 (Amersham Pharmacia Biotech). The reverse transcription reaction is performed in a 25 ml volume containing 200 ng poly(A)⁺ RNA with GEMBRIGHT kits (Incyte). Specific control poly(A)⁺ RNAs are synthesized by in vitro transcription from non-coding yeast genomic DNA. After incubation at 37° C for 2 hr, each reaction sample (one with Cy3 and another with Cy5 labeling) is treated with 2.5 ml of 0.5M sodium hydroxide and incubated for 20 minutes at 85° C to stop the reaction and degrade the RNA. Samples are purified using two successive CHROMA SPIN 30 gel filtration spin columns (CLONTECH Laboratories, Inc. (CLONTECH), Palo Alto CA) and after combining, both reaction samples are ethanol precipitated using 1 ml of glycogen (1 mg/ml), 60 ml sodium acetate, and 300 ml of 100% ethanol. The sample is

then dried to completion using a SpeedVAC (Savant Instruments Inc., Holbrook NY) and resuspended in 14 µl 5X SSC/0.2% SDS.

Microarray Preparation

Sequences of the present invention are used to generate array elements. Each array element is amplified from bacterial cells containing vectors with cloned cDNA inserts. PCR amplification uses primers complementary to the vector sequences flanking the cDNA insert. Array elements are amplified in thirty cycles of PCR from an initial quantity of 1-2 ng to a final quantity greater than 5 µg. Amplified array elements are then purified using SEPHACRYL-400 (Amersham Pharmacia Biotech).

Purified array elements are immobilized on polymer-coated glass slides. Glass microscope slides (Corning) are cleaned by ultrasound in 0.1% SDS and acetone, with extensive distilled water washes between and after treatments. Glass slides are etched in 4% hydrofluoric acid (VWR Scientific Products Corporation (VWR), West Chester PA), washed extensively in distilled water, and coated with 0.05% aminopropyl silane (Sigma) in 95% ethanol. Coated slides are cured in a 110°C oven.

Array elements are applied to the coated glass substrate using a procedure described in US Patent No. 5,807,522, incorporated herein by reference. 1 µl of the array element DNA, at an average concentration of 100 ng/µl, is loaded into the open capillary printing element by a high-speed robotic apparatus. The apparatus then deposits about 5 nl of array element sample per slide.

Microarrays are UV-crosslinked using a STRATALINKER UV-crosslinker (Stratagene). Microarrays are washed at room temperature once in 0.2% SDS and three times in distilled water. Non-specific binding sites are blocked by incubation of microarrays in 0.2% casein in phosphate buffered saline (PBS) (Tropix, Inc., Bedford MA) for 30 minutes at 60°C followed by washes in 0.2% SDS and distilled water as before.

Hybridization

Hybridization reactions contain 9 µl of sample mixture consisting of 0.2 µg each of Cy3 and Cy5 labeled cDNA synthesis products in 5X SSC, 0.2% SDS hybridization buffer. The sample mixture is heated to 65°C for 5 minutes and is aliquoted onto the microarray surface and covered with an 1.8 cm² coverslip. The arrays are transferred to a waterproof chamber having a cavity just slightly larger than a microscope slide. The chamber is kept at 100% humidity internally by the addition of 140 µl of 5X SSC in a corner of the chamber. The chamber containing the arrays is incubated for about 6.5 hours at 60°C. The arrays are washed for 10 min at 45°C in a first wash buffer (1X SSC, 0.1% SDS), three times for 10 minutes each at 45°C in a second wash buffer (0.1X SSC), and dried.

Detection

Reporter-labeled hybridization complexes are detected with a microscope equipped with an Innova 70 mixed gas 10 W laser (Coherent, Inc., Santa Clara CA) capable of generating spectral lines at 488 nm for excitation of Cy3 and at 632 nm for excitation of Cy5. The excitation laser light is focused on the array using a 20X microscope objective (Nikon, Inc., Melville NY). The slide
5 containing the array is placed on a computer-controlled X-Y stage on the microscope and raster-scanned past the objective. The 1.8 cm x 1.8 cm array used in the present example is scanned with a resolution of 20 micrometers.

In two separate scans, a mixed gas multiline laser excites the two fluorophores sequentially. Emitted light is split, based on wavelength, into two photomultiplier tube detectors (PMT R1477,
10 Hamamatsu Photonics Systems, Bridgewater NJ) corresponding to the two fluorophores. Appropriate filters positioned between the array and the photomultiplier tubes are used to filter the signals. The emission maxima of the fluorophores used are 565 nm for Cy3 and 650 nm for Cy5. Each array is typically scanned twice, one scan per fluorophore using the appropriate filters at the laser source, although the apparatus is capable of recording the spectra from both fluorophores simultaneously.

15 The sensitivity of the scans is typically calibrated using the signal intensity generated by a cDNA control species added to the sample mixture at a known concentration. A specific location on the array contains a complementary DNA sequence, allowing the intensity of the signal at that location to be correlated with a weight ratio of hybridizing species of 1:100,000. When two samples from different sources (e.g., representing test and control cells), each labeled with a different
20 fluorophore, are hybridized to a single array for the purpose of identifying genes that are differentially expressed, the calibration is done by labeling samples of the calibrating cDNA with the two fluorophores and adding identical amounts of each to the hybridization mixture.

The output of the photomultiplier tube is digitized using a 12-bit RTI-835H analog-to-digital (A/D) conversion board (Analog Devices, Inc., Norwood MA) installed in an IBM-compatible PC
25 computer. The digitized data are displayed as an image where the signal intensity is mapped using a linear 20-color transformation to a pseudocolor scale ranging from blue (low signal) to red (high signal). The data is also analyzed quantitatively. Where two different fluorophores are excited and measured simultaneously, the data are first corrected for optical crosstalk (due to overlapping emission spectra) between the fluorophores using each fluorophore's emission spectrum.

30 A grid is superimposed over the fluorescence signal image such that the signal from each spot is centered in each element of the grid. The fluorescence signal within each element is then integrated to obtain a numerical value corresponding to the average intensity of the signal. The software used for signal analysis is the GEMTOOLS gene expression analysis program (Incyte).

XI. Complementary Polynucleotides

Sequences complementary to the PKIN-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring PKIN. Although use of oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides are designed using OLIGO 4.06 software (National Biosciences) and the coding sequence of PKIN. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to the PKIN-encoding transcript.

XII. Expression of PKIN

Expression and purification of PKIN is achieved using bacterial or virus-based expression systems. For expression of PKIN in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac* (*tac*) hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express PKIN upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of PKIN in eukaryotic cells is achieved by infecting insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding PKIN by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945.)

In most expression systems, PKIN is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from PKIN at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak). 6-

His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, supra, ch. 10 and 16). Purified PKIN obtained by these methods can be used directly in the assays shown in Examples XVI, XVII, and XVIII where applicable.

5 XIII. Functional Assays

PKIN function is assessed by expressing the sequences encoding PKIN at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include PCMV SPORT (Life Technologies) and PCR3.1 (Invitrogen, Carlsbad CA), both of which
10 contain the cytomegalovirus promoter. 5-10 μ g of recombinant vector are transiently transfected into a human cell line, for example, an endothelial or hematopoietic cell line, using either liposome formulations or electroporation. 1-2 μ g of an additional plasmid containing sequences encoding a marker protein are co-transfected. Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the
15 recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; Clontech), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated, laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties. FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include
20 changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated
25 Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M.G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of PKIN on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding PKIN and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human
30 immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding PKIN and other genes of interest can be analyzed by northern analysis or microarray techniques.

XIV. Production of PKIN Specific Antibodies

PKIN substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) *Methods Enzymol.* 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

Alternatively, the PKIN amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, *supra*, ch. 11.)

Typically, oligopeptides of about 15 residues in length are synthesized using an ABI 431A peptide synthesizer (Applied Biosystems) using FMOC chemistry and coupled to KLH (Sigma-Aldrich, St. Louis MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, 1995, *supra*.) Rabbits are immunized with the oligopeptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for anti-peptide and anti-PKIN activity by, for example, binding the peptide or PKIN to a substrate, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG.

XV. Purification of Naturally Occurring PKIN Using Specific Antibodies

Naturally occurring or recombinant PKIN is substantially purified by immunoaffinity chromatography using antibodies specific for PKIN. An immunoaffinity column is constructed by covalently coupling anti-PKIN antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing PKIN are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PKIN (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/PKIN binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and PKIN is collected.

XVI. Identification of Molecules Which Interact with PKIN

PKIN, or biologically active fragments thereof, are labeled with ¹²⁵I Bolton-Hunter reagent. (See, e.g., Bolton A.E. and W.M. Hunter (1973) *Biochem. J.* 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled PKIN, washed, and any wells with labeled PKIN complex are assayed. Data obtained using different concentrations of PKIN are used to calculate values for the number, affinity, and association of PKIN with the candidate molecules.

Alternatively, molecules interacting with PKIN are analyzed using the yeast two-hybrid system as described in Fields, S. and O. Song (1989) Nature 340:245-246, or using commercially available kits based on the two-hybrid system, such as the MATCHMAKER system (Clontech).

PKIN may also be used in the PATHCALLING process (CuraGen Corp., New Haven CT) which employs the yeast two-hybrid system in a high-throughput manner to determine all interactions between the proteins encoded by two large libraries of genes (Nandabalan, K. et al. (2000) U.S. Patent No. 6,057,101).

XVII. Demonstration of PKIN Activity

Generally, protein kinase activity is measured by quantifying the phosphorylation of a protein substrate by PKIN in the presence of gamma-labeled ^{32}P -ATP. PKIN is incubated with the protein substrate, ^{32}P -ATP, and an appropriate kinase buffer. The ^{32}P incorporated into the substrate is separated from free ^{32}P -ATP by electrophoresis and the incorporated ^{32}P is counted using a radioisotope counter. The amount of incorporated ^{32}P is proportional to the activity of PKIN. A determination of the specific amino acid residue phosphorylated is made by phosphoamino acid analysis of the hydrolyzed protein.

In one alternative, protein kinase activity is measured by quantifying the transfer of gamma phosphate from adenosine triphosphate (ATP) to a serine, threonine or tyrosine residue in a protein substrate. The reaction occurs between a protein kinase sample with a biotinylated peptide substrate and gamma ^{32}P -ATP. Following the reaction, free avidin in solution is added for binding to the biotinylated ^{32}P -peptide product. The binding sample then undergoes a centrifugal ultrafiltration process with a membrane which will retain the product-avidin complex and allow passage of free gamma ^{32}P -ATP. The reservoir of the centrifuged unit containing the ^{32}P -peptide product as retentate is then counted in a scintillation counter. This procedure allows assay of any type of protein kinase sample, depending on the peptide substrate and kinase reaction buffer selected. This assay is provided in kit form (ASUA, Affinity Ultrafiltration Separation Assay, Transbio Corporation, Baltimore MD, U.S. Patent No. 5,869,275). Suggested substrates and their respective enzymes are as follows: Histone H1 (Sigma) and p34^{cdc2}kinase, Annexin I, Angiotensin (Sigma) and EGF receptor kinase, Annexin II and *src* kinase, ERK1 & ERK2 substrates and MEK, and myelin basic protein and ERK (Pearson, J.D. et al. (1991) Methods Enzymol. 200:62-81).

In another alternative, protein kinase activity of PKIN is demonstrated in vitro in an assay containing PKIN, 50 μl of kinase buffer, 1 μg substrate, such as myelin basic protein (MBP) or synthetic peptide substrates, 1 mM DTT, 10 μg ATP, and 0.5 μCi [γ - ^{33}P]ATP. The reaction is incubated at 30°C for 30 minutes and stopped by pipetting onto P81 paper. The unincorporated [γ - ^{33}P]ATP is removed by washing and the incorporated radioactivity is measured using a radioactivity scintillation

counter. Alternatively, the reaction is stopped by heating to 100°C in the presence of SDS loading buffer and visualized on a 12% SDS polyacrylamide gel by autoradiography. Incorporated radioactivity is corrected for reactions carried out in the absence of PKIN or in the presence of the inactive kinase, K38A.

5 In yet another alternative, adenylate kinase or guanylate kinase activity may be measured by the incorporation of ^{32}P from gamma-labeled ^{32}P -ATP into ADP or GDP using a gamma radioisotope counter. The enzyme, in a kinase buffer, is incubated together with the appropriate nucleotide mono-phosphate substrate (AMP or GMP) and ^{32}P -labeled ATP as the phosphate donor. The reaction is incubated at 37°C and terminated by addition of trichloroacetic acid. The acid extract is neutralized
10 and subjected to gel electrophoresis to separate the mono-, di-, and triphosphonucleotide fractions. The diphosphonucleotide fraction is cut out and counted. The radioactivity recovered is proportional to the enzyme activity.

In yet another alternative, other assays for PKIN include scintillation proximity assays (SPA), scintillation plate technology and filter binding assays. Useful substrates include recombinant proteins
15 tagged with glutathione transferase, or synthetic peptide substrates tagged with biotin. Inhibitors of PKIN activity, such as small organic molecules, proteins or peptides, may be identified by such assays.

XVIII. Enhancement/Inhibition of Protein Kinase Activity

Agonists or antagonists of PKIN activation or inhibition may be tested using assays described in section XVII. Agonists cause an increase in PKIN activity and antagonists cause a decrease in PKIN
20 activity.

Various modifications and variations of the described methods and systems of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with certain embodiments, it should be
25 understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

Table 1

Incyte Project ID	Polypeptide SEQ ID NO:	Incyte Polypeptide ID	Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID
2011384	1	2011384CD1	27	2011384CB1
2004888	2	2004888CD1	28	2004888CB1
2258952	3	2258952CD1	29	2258952CB1
7473244	4	7473244CD1	30	7473244CB1
1242491	5	1242491CD1	31	1242491CB1
2634875	6	2634875CD1	32	2634875CB1
3951059	7	3951059CD1	33	3951059CB1
7395890	8	7395890CD1	34	7395890CB1
7475546	9	7475546CD1	35	7475546CB1
7477076	10	7477076CD1	36	7477076CB1
1874092	11	1874092CD1	37	1874092CB1
4841542	12	4841542CD1	38	4841542CB1
7472695	13	7472695CD1	39	7472695CB1
7477966	14	7477966CD1	40	7477966CB1
7163416	15	7163416CD1	41	7163416CB1
7472822	16	7472822CD1	42	7472822CB1
7477486	17	7477486CD1	43	7477486CB1
3773709	18	3773709CD1	44	3773709CB1
7477204	19	7477204CD1	45	7477204CB1
3016969	20	3016969CD1	46	3016969CB1
063497	21	063497CD1	47	063497CB1
1625436	22	1625436CD1	48	1625436CB1
3330646	23	3330646CD1	49	3330646CB1
3562763	24	3562763CD1	50	3562763CB1
621293	25	621293CD1	51	621293CB1
7480774	26	7480774CD1	52	7480774CB1

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO:	Probability score	GenBank Homolog
1	2011384CD1	g404634	4.50E-60	[Mus musculus] serine/threonine kinase (Bielke, W. et al (1994) Gene 139 (2), 235-239)
2	2004888CD1	g13540326 g2983205	1.00E-159 2.70E-08	[fl][Homo sapiens] serine/threonine kinase FKSG82 [Aquifex aeolicus] ser/thr protein kinase (Deckert, G. et al (1998) Nature 392 (6674), 353-358)
3	2258952CD1	g13603881 g3766209	0 0	[fl][Homo sapiens] serine/threonine kinase 31 (Wang, P.J. et al, (2001) Nat. Genet. 27 (4), 422-426) [Mus musculus] IRE1 (Wang, X.Z. et al (1998) EMBO J. 17 (19), 5708-5717)
4	7473244CD1	g2052189	0	[Rattus norvegicus] serine/threonine kinase
5	1242491CD1	g2253010	8.40E-25	[Arabidopsis thaliana] MAP3K delta-1 protein kinase (Jouannic, S. et al (1999) Gene 229 (1-2), 171-181)
6	2634875CD1	g13194657 g165506	0 1.50E-272	[fl][Homo sapiens] skeletal myosin light chain kinase [Oryctolagus cuniculus] myosin light chain kinase (EC 2.7.1.1-) (Herring, B.P. et al (1990) J. Biol. Chem. 265, 1724- 1730)
7	3951059CD1	g3599507	5.00E-235	[Mus musculus] rho/rac-interacting citron kinase short isoform (Di Cunto, F. et al (1998) J. Biol. Chem. 273 (45), 29706-29711)
8	7395890CD1	g5815139	0	[Mus musculus] nuclear body associated kinase 1a
9	7475546CD1	g3435114	1.80E-50	[Homo sapiens] serine/threonine kinase ULK1 (Kuroyanagi, H. et al (1998) Genomics 51 (1), 76-85)
10	7477076CD1	g854733	6.20E-198	[Rattus norvegicus] casein kinase 1 gamma 1 isoform
11	1874092CD1	g2511715	4.00E-25	[Arabidopsis thaliana] putative phosphatidylinositol-4- phosphate
12	4841542CD1	g927732	3.30E-67	[Saccharomyces cerevisiae] Snf1p: serine/threonine protein kinase:
13	7472695CD1	g1498250	1.10E-53	[Dictyostelium discoideum] myosin light chain kinase (Tan, J.L. et al (1991) J. Biol. Chem. 266, 16044-16049)
14	7477966CD1	g12830367 g3766209	0 0	[fl][Homo sapiens] serine/threonine kinase 33 [Mus musculus] IRE1 (Wang, X.Z. et al (1998) EMBO J. 17 (19), 5708-5717)

Table 2 (cont.)

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO:	Probability score	GenBank Homolog
15	7163416CD1	g7649810 g11691855	2.10E-135 0	[Homo sapiens] protein kinase PAK5 [fl][Homo sapiens] pak5 protein
16	7472822CD1	g5081459	3.70E-241	[Danio rerio] p55-related MAGUK protein DLG3
17	7477486CD1	g3217028	0	[5' incom][Homo sapiens] putative serine/threonine protein kinase (Stanchi, F. et al (2001) Yeast 18 (1), 69-80)
18	3773709CD1	g3986088	6.70E-78	[Pyrococcus kodakaraensis] Glycerol Kinase
19	7477204CD1	g992672	7.30E-129	[Homo sapiens] G protein-coupled receptor kinase GRK4- beta (Premont, R.T. et al (1996) J. Biol. Chem. 271 (11), 6403-6410)
		g4001826	0	[fl][Spermophilus tridecemlineatus] G protein-coupled receptor kinase GRK7 (Weiss, E.R. et al (1998) Mol. Vis. 4, 27)
20	3016969CD1	g4521278	4.70E-45	[Homo sapiens] Trad (Kawai, T. et al (1999) Gene 227 (2), 249-255)
21	63497CD1	g1213224	0	[Rattus norvegicus] SNF1-related kinase (Becker, W. et al (1996) Eur. J. Biochem. 235 (3), 736- 743)
22	1625436CD1	g4096108 g206152	1.10E-252 0	[Homo sapiens] proline rich calmodulin-dependent protein kinase [fl][Rattus norvegicus] calmodulin-dependent protein kinase II gamma subunit (EC 2.7.1.37) (Tobimatsu, T. et al (1988) J. Biol. Chem. 263, 16082- 16086)
23	3330646CD1	g406058	0	[Mus musculus] protein kinase (Walden, P.D. et al (1993) Mol. Cell. Biol. 13, 7625- 7635)
24	3562763CD1	g12830335 g1510182	0 9.80E-18	[5' incom][Homo sapiens] bA55008.2 (novel protein kinase) [Mus musculus] cyclin-dependent kinase 5 (Ishizuka, T. et al (1995) Gene 166 (2), 267-271)
25	621293CD1	g2649941	4.50E-23	[Archaeoglobus fulgidus] adenylate kinase (adk) (Klenk, H.P. et al (1997) Nature 390 (6658), 364-370)
26	7480774CD1	g2463542	0	"[Homo sapiens] inositol 1,4,5-trisphosphate 3-kinase"

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
1	2011384CD1	273	Y12 Y23 T17 S144 T30 S31 S237 S253		PROTEIN KINASE DOMAIN DM00004 P27448 58-297: R16-R255 Eukaryotic protein kinase domain pkinase: Y12-L267 Protein kinases signatures and profile, protein_kinase_tyr.prf: Q111-G163 Protein Kinase ATP binding site: I18-K41 Protein Kinase (serine/threonine): L131-L143 Tyrosine kinase catalytic domain signature: PR00109:Y125-L143 Y193-S215 Eukaryotic protein kinase domain pkinase: P135-L228 DM00004 P54744 13-263 PROTEIN KINASE DOMAIN: P113-L228 (P=1.1e-06) PROTEIN KINASE DOMAIN DM00004 Q09499 536-784:P534-A784 KINASE; THREONINE; ATP; SERINE; DM06305 Q09499 786-924:V787-Y922 PROTEIN KINASE/ENDORIBONULCEASE PUTATIVE SERINE/THREONINE PROTEIN KINASE C41C4.4 CHROMOSOME II PRECURSOR TRANSFERASE PD152704:T170-L395,L61-E163	BLAST_DOMO HMMER_PFAM PROFILESKAN MOTIFS MOTIFS BLIMPS_PRINTS HMMER_PFAM BLAST_DOMO BLAST_DOMO BLAST_PRODUM
2	2004888CD1	329	S190 S50 S51 T141 Y302			
3	2258952CD1	938	S207 S299 S500 S503 S580 S609 S65 S714 S814 S852 S857 T116 T128 T147 T175 T188 T202 T345 T55 T592 T658 T84 T895 T905 T936 Y146	N200		

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
3					SERINE/THREONINE PROTEIN KINASE PRECURSOR TRANSMEMBRANE SIGNAL TRANSFERASE ATP-BINDING PROTEIN IRE1 GLYCOPROTEIN PD032590:W794-Y922 Tyrosine kinase catalytic domain PR00109: H639-I657, G694-L704, V716-D738 Protein kinases signatures and profile protein_kinase_tyr.prf: E625-G682 Eukaryotic protein kinase domain pkinase: F532-F793 Protein_Kinase serine/threonine: I645-I657	BLAST_PRODOR BLIMPS_PRINTS
4	7473244CD1	795	S140 S2 S301 S35 S423 S468 S485 S486 S49 S524 S546 S609 S666 S671 S699 S705 S710 S776 T128 T19 T282 T324 T333 T437 T504 T511 T568 T581 T648 T657 T676 T680 T82 T9	N17 N331 N397 N398	Protein kinases signatures and profile protein_kinase_tyr.prf: Y133-G210 Eukaryotic protein kinase domain pkinase: Y60-M311 PROTEIN KINASE DOMAIN DM00004 P27448 58-297:L62-L302	PROFILESSCAN HMMER_PFAM BLAST_DOMO

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
4					KINASE SERINE/THREONINE PUTATIVE PROTEIN TRANSFERASE ATP-BINDING SERINE/THREONINE PUTATIVE KIN1 EMK PAR1 PD004300:G682-L795 SERINE/THREONINE KINASE PD119193:I594-P665 KINASE SERINE/THREONINE PUTATIVE TRANSFERASE ATP-BINDING PROTEIN EMK P78 CDC25C PD008571:S412-S595 KINASE SERINE/THREONINE PUTATIVE PROTEIN TRANSFERASE ATP-BINDING PROTEIN PAR1 KP78 EMK PD005838:M311-R411 Tyrosine kinase catalytic domain PR00109: M136-V149, Y172-L190, V238-Q260 Protein_Kinase_ATP binding site: I66-K89 Protein_Kinase serine/threonine: I178-L190	BLAST_PRODOM BLAST_PRODOM BLAST_PRODOM BLAST_PRODOM BLIMPS_PRINTS MOTIFS MOTIFS
5	1242491CD1	656	S309 S42 S540 S569 S583 S594 S654 T270 T303 T319 T366 T408 T439 T509 T526 T570 T609 T612 T623 T653	N293 N424 N437	Eukaryotic protein kinase domain: L14-V257 Protein kinases signatures and profile: L99-Q151 Protein kinases ATP-binding region signature: L14-K35 Serine/Threonine protein kinases active-site signature: I119-L131	HMMER_PFAM PROFILES SCAN MOTIFS MOTIFS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
5					Tyrosine kinase catalytic domain signature PR00109:M76-Q89, Y113-L131, A183-G205, P232-S254 PROTEIN KINASE DOMAIN DM00004 P42679 236-470:L14-P252 DM00004 I49621 195-428:L14-P252 DM00004 I38044 100-349:L13-P252 DM00004 Q05609 553-797:L14-T197, L14-T253	BLIMPS_PRINTS BLAST_DOMO
6	2634875CD1	596	S107 S143 S157 S159 S184 S203 S235 S397 S460 S586 S59 T17 T224 T247 T301 T320 T351 T379 T49 Y376	N278 N416	Eukaryotic protein kinase domain: M285-L540 Tyrosine kinase catalytic domain signature PR00109:M359-V372, F396-C414, T463-D485 Protein kinases ATP-binding region signature: L291-K314 Serine/Threonine protein kinases active-site signature: V402-C414 KINASE MYOSIN LIGHT CHAIN SKELETAL MUSCLE MLCK TRANSFERASE SERINE/THREONINE CALMODULIN BINDING PD036174:A95-M285 PD027051:L540-V596 PD029157:A2-R82, A2-S90	HMMER_PFAM BLIMPS_PRINTS MOTIFS MOTIFS BLAST_PRODOM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
6					PROTEIN KINASE DOMAIN DM00004 P07313 298-541: S287-A531 DM00004 JN0583 727-969: K288-N530 DM00004 S07571 5152-5396: E289-M529 DM00004 P53355 15-257: E289-M529	BLAST_DOMO
7	3951059CD1	497	S140 S248 S308 S361 S381 S386 S410 S436 S445 S490 S81 S93 T279 T378 T83		Eukaryotic protein kinase domain: F97-F360 Protein kinase C terminal domain: S361-E390 Tyrosine kinase catalytic domain signature PR00109: M174-N187, S211-V229 Protein kinases ATP-binding region signature: V103-K126 Serine/Threonine protein kinases active-site signature: Y217-V229 RHO/RACINTERACTING CITRON KINASE SHORT ISOFORM PD154232: S422-V468 PD154360: M1-M43 KINASE RHO ASSOCIATED COILED COIL PROTEIN FORMING RHO/RAC INTERACTING CITRON ALPHA PD007970: Q32-D96	HMMER_PFAM HMMER_PFAM BLIMPS_PRINTS MOTIFS MOTIFS BLAST_PRODOM BLAST_PRODOM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
7					PROTEIN KINASE DOMAIN DM00004 Q09013 83-336: V99-L349 DM00004 S42867 75-498: S101-G241, I258-S445 DM00004 S42864 41-325: E98-G241, N249-L349, D96-T153 DM00004 P38679 238-527:L102-G241, I258-L349, E86-A124	BLAST_DOMO
8	7395890CD1	1171	S121 S135 S178 S180 S254 S27 S37 S405 S649 S773 S774 S783 S788 S804 S865 S970 T119 T172 T221 T431 T450 T483 T517 T839 T867 T893 T995 T1022 S1027 S1099 Y443 Y468	N140 N157 N271 N480 N562 N579 N786 N963 N978 N1012	Eukaryotic protein kinase domain: Y199-P420, R498-V527 Tyrosine kinase catalytic domain signature PR00109:K314-L332 Protein kinases ATP-binding region signature: L205-K228 Serine/Threonine protein kinases active-site signature: L320-L332 PROTEIN KINASE NUCLEAR HOMEO DOMAIN INTERACTING DNA-BINDING SERINE/THREONINE PD141983:A573-C933 PD150874:A993-I1171 PROTEIN KINASE NUCLEAR SERINE/THREONINE HOMEO DOMAIN INTERACTING DNA-BINDING SERINE/THREONINE F20B6.8 PD042899:L425-P574 HOMEO DOMAIN INTERACTING PROTEIN KINASE 2 DNA-BINDING NUCLEAR PROTEIN PD184491:E872-P961	HMMER_PFAM BLIMPS_PRINTS MOTIFS MOTIFS BLAST_PRODOM BLAST_PRODOM BLAST_PRODOM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
8					PROTEIN KINASE DOMAIN DM00004 P14680 371-694: V201-P518 DM00004 Q09815 519-804: E200-L473, F500-T517 DM00004 P49657 101-409: L205-P518 DM00004 Q09690 700-985: E200-P444, F500-P518	BLAST_DOMO
9	7475546CD1	470	S134 S146 S165 S217 S219 S227 S256 S260 S339 S361 S406 S447 S462 T105 T17 T37 T61	N132	Eukaryotic protein kinase domain: F14-V270 Tyrosine kinase catalytic domain signature PR00109:M91-H104, F127-L145, L239-F261 Protein kinases signatures and profile: V113-P166 Protein kinases ATP-binding region signature: L20-K44 Serine/Threonine protein kinases active-site signature: I133-L145 KINASE PROTEIN TRANSFERASE ATP BINDING SERINE/THREONINE RECEPTOR TYROSINE PRECURSOR TRANSMEMBRANE PD000001:S176-P255, I15-F93, P237-W269, F117-M164, L20-K34 PROTEIN KINASE DOMAIN DM00004 P53104 26-315: P151-F261, E18-E111, F117-S147 DM00004 S54788 154-400:L20-S260 DM00004 P27448 58-297: L16-R258 DM00004 P49673 31-267: L20-I259	HMMER_PFAM BLTPS_PRINTS PROFILES SCAN MOTIFS MOTIFS BLAST_PROD OM BLAST_DOMO

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
10	7477076CD1	422	S124 S150 S229 S96 T137 T14 T199 T214 T258 T269 T273 T355 T374 T417		Eukaryotic protein kinase domain pkinase: F44-E276 Protein kinases signatures and profile: T140-P197 Protein kinases ATP-binding region signature: I50-K73 Serine/Threonine protein kinases active-site signature: L160-I172 CASEIN KINASE I GAMMA ISOFORM TRANSFERASE SERINE/THREONINE ATP BINDING MULTIGENE PD015080:F315-T393 CASEIN KINASE I, GAMMA 1 ISOFORM EC 2.7.1. CKI GAMMA TRANSFERASE SERINE/THREONINE PROTEIN ATP BINDING MULTIGENE PD049080:M1-N43 PROTEIN KINASE DOMAIN DM00004 A56711 46-303:V46-Y304 DM00004 C56711 45-301:V46-Y304 DM00004 B56711 48-303:V46-Y304 DM00004 D56406 31-276:V46-V293	HMMER_PFAM
11	1874092CD1	240	S121 S132 S78 T197 T84		PROTEIN PHOSPHATIDYL INOSITOL 4-PHOSPHATE 5-KINASE PUTATIVE T22C1.7 ISOLOG ATP1P5K1 T4C15.16 PD149995: L13-D204	BLAST_PRODOR

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
12	4841542CD1	594	S108 S114 S293 S297 S305 S306 S339 S343 S382 S40 S427 S48 S489 S572 S88 S99 T193 T255 T259 T357 T477 T544 T582 Y425	N542 N87	KINASE PROTEIN TRANSFERASE ATP-BINDING SERINE/THREONINE PROTEIN PHOSPHORYLATION RECEPTOR TYROSINE PROTEIN PRECURSOR TRANSMEMBRANE PD000001: K3-S163, S178-F216, P236-W268 (P=1.2e-09) PROTEIN KINASE DOMAIN DM00004 P27448 58-297: L22-L260 DM00004 P06782 57-296: L22-L260 DM00004 JC1446 20-261: T24-L260 DM00004 P54645 17-258: E23-L260 Tyrosine kinase catalytic domain signature PR00109: M95-S108, Y131-L149, V197-H219 Eukaryotic protein kinase domain pkinase: Y19-V269 Protein_Kinase_ATP L25-K47 Protein_Kinase_Serine/Threonine V137-L149	BLAST_PRODOR BLAST_DOMO BLIMPS_PRINTS HMMER_PFAM MOTIFS MOTIFS HMMER_PFAM
13	7472695CD1	473	S128 S170 S208 S233 S255 S285 S30 S308 S347 S366 S379 S39 S400 S432 S46 T143 T29 T330 T371 T399 T409 T418 T469 T93	N172 N370 N397 N54	Eukaryotic protein kinase domain pkinase: Y75-L340	HMMER_PFAM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
13					<p>PROTEIN KINASE DOMAIN</p> <p>DM00004 S57347 21-266: F77-T330</p> <p>DM00004 S46283 13-259: G78-A331</p> <p>DM00004 S54788 154-400: G78-A331</p> <p>DM00004 P28583 35-282: G78-A331</p> <p>KINASE PROTEIN TRANSFERASE ATP-BINDING SERINE/THREONINE PROTEIN PHOSPHORYLATION RECEPTOR TYROSINE PROTEIN PRECURSOR TRANSMEMBRANE</p> <p>PD000001: D197-L299, R79-D156</p> <p>Tyrosine kinase catalytic domain</p> <p>PR00109: M151-D164, Y187-V205, C263-S285, T143-R165</p> <p>Phosphorylase kinase family</p> <p>PR101049: D164-I184</p> <p>Protein_Kinase_ATP</p> <p>L81-K104</p> <p>Protein_Kinase_Serine/Threonine</p> <p>I193-V205</p> <p>protein_kinase_tyrosine.profile:</p> <p>E173-A228</p>	BLAST_DOMO
14	7477966CD1	947	S207 S299 S508 S511 S589 S618 S65 S723 S823 S861 S866 T116 T128 T147 T175 T188 T202 T345 T55 T601 T667 T84 T904 T914 T945 Y146	N200	<p>Eukaryotic protein kinase domain</p> <p>pkinae:</p> <p>F541-F802</p>	HMMER_PFAM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
14					<p>PROTEIN KINASE DOMAIN DM00004 Q09499 536-784: P543-A793 DM00004 P32361 676-970: V546-Q714, T722-A793</p> <p>do KINASE; THREONINE; ATP; SERINE; DM06305 Q09499 786-924: V796-Y931 DM06305 P32361 972-1114: Q795-L928</p> <p>PROTEIN KINASE/ENDORIBONULCEASE PUTATIVE SERINE/THREONINE PROTEIN KINASE C41C4.4 CHROMOSOME II PRECURSOR TRANSFERASE PD152704: T170-L395, L61-E163</p> <p>SERINE/THREONINE PROTEIN KINASE PRECURSOR TRANSMEMBRANE SIGNAL TRANSFERASE ATP-BINDING PROTEIN IRE1 GLYCOPROTEIN PD032590: W803-Y931</p> <p>Tyrosine kinase catalytic domain signature PR00109: H648-I666, G703-L713, V725-D747</p> <p>Phosphorylase kinase family signature PR01049: P794-R805</p> <p>Protein_Kinase_Serine/Threonine: I654-I666 protein_kinase_tyrosine.profile: E634-G691</p>	<p>BLAST_DOMO</p> <p>BLAST_DOMO</p> <p>BLAST_PRODOM</p> <p>BLAST_PRODOM</p> <p>BLIMPS_PRINTS</p> <p>BLIMPS_PRINTS</p> <p>MOTIFS</p> <p>PROFILES SCAN</p> <p>HMMER_PFAM</p>
15	7163416CD1	641	S107 S135 S165 S189 S248 S255 S276 S290 S332 S351 S429 S560 S624 T106 T107 T124 T212 T238 T24 T322 T46 T505 T580 T99	N288	<p>Eukaryotic protein kinase domain pkinae: L407-Y601</p>	

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosyla- tion Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
15					<p>PROTEIN KINASE DOMAIN</p> <p>DM00004 P35465 271-510: Y410-S628</p> <p>DM00004 I49376 270-509: K412-S628</p> <p>DM00004 Q03497 622-861: V411-S628</p> <p>DM00004 P50527 388-627: S409-S628</p> <p>KINASE SERINE/THREONINE PROTEIN TRANSFERASE ATP-BINDING PROTEIN PHOSPHORYLATION P21 ACTIVATED ACTIVATED HOMOLOG SYNDROME</p> <p>PD002852: I12-L44 (P=3.0e-06)</p> <p>Tyrosine kinase catalytic domain signature PR00109: M481-S494, Y516-L534, G563-I573, V582-D604</p> <p>Protein_Kinase_ATP I413-K436</p>	BLAST_DOMO
16	7472822CD1	576	<p>S109 S136 S220</p> <p>S255 S266 S31</p> <p>S313 S318 S323</p> <p>S327 S336 S451</p> <p>S505 S506 S8</p> <p>T152 T213 T333</p> <p>T353 T364 T403</p> <p>T447 T470 T497</p> <p>T517 T557 Y440</p> <p>Y482 Y59</p>	N334	<p>GUANYLATE KINASE</p> <p>DM00755 A57653 370-570: P359-P570</p> <p>DM00755 I38757 709-898: R369-P570</p> <p>DM00755 S32545 1-196: R369-K556</p> <p>DM00755 P31007 765-954: R369-P570</p>	<p>BLAST_PRODOR</p> <p>BLIMPS_PRINTS</p> <p>MOTIFS</p> <p>HMMER_PFAM</p> <p>BLAST_DOMO</p>

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosyla- tion Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
16					PROTEIN DOMAIN SH3 KINASE GUANYLATE TRANSFERASE ATP-BINDING REPEAT GMP MEMBRANE PD001338: T403-E496 PROTEIN SH3 DOMAIN PERIPHERAL PLASMA MEMBRANE CALMODULIN BINDING CASK CAMGUK CALCIUM PD008238: M1-I139 PROTEIN MAGUK P55 SUBFAMILY MEMBER DISCS LARGE HOMOLOG SH3 DOMAIN PD152180: K230-R297 PROTEIN MAGUK P55 SUBFAMILY MEMBER MPP3 DISCS LARGE HOMOLOG SH3 PD090357: S318-T403 Guanylate kinase protein BL00856: V400-I420, D428-R475 SH3 domain signature PR00452: R284-R296, M231-P241, A252- Q267 PDZ domain (Also known as DHR or GLGF). PDZ: I139-G219 SH3 domain SH3: M231-R296 Guanylate_Kinase: T403-I420 signal_cleavage: M1-S31	BLAST_PRODOM BLAST_PRODOM BLAST_PRODOM BLAST_PRODOM BLIMPS_BLOCKS BLIMPS_PRINTS HMMER_PFAM HMMER_PFAM MOTIFS SPSCAN

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
17	7477486CD1	794	S130 S158 S19 S201 S291 S327 S357 S379 S420 S443 S463 S512 S524 S571 S579 S602 S635 S659 S684 S692 S715 S731 S774 T145 T433 T488 T539 T591		<p>PROTEIN KINASE DOMAIN DM00004 P34244 82-359: I71-S291 DM00004 JC1446 20-261: R51-L292 DM00004 P54645 17-258: L52-L292 DM00004 A53621 18-258: L52-L292</p> <p>KINASE PROTEIN TRANSFERASE ATP-BINDING SERINE/THREONINE PROTEIN PHOSPHORYLATION RECEPTOR TYROSINE PROTEIN PRECURSOR TRANSMEMBRANE PD000001: R42-L138, L144-A194 S209-F247, I270-L302 Tyrosine kinase catalytic domain signature PR00109: L126-V139, F162-L180, A228-D250, I270-L292 Eukaryotic protein kinase domain pkinase: Y50-Y301 Protein_Kinase_ATP L56-K79 Protein_Kinase_Serine/Threonine: I168-L180 protein_kinase_tyrosine.profile: K120-S201</p>	BLAST_DOMO
18	3773709CD1	504	S117 S142 S152 S169 S232 S339 T274 T333 T375 T459 T6 T96 Y17	N131 N132 N178 N216	<p>XYLULOKINASE DM02388 P18157 1-492: F20-M498 GLYCEROL 3PHOSPHOTRANSFERASE GLYCEROKINASE GK PD001007: G239-A448 SIMILAR TO GLYCEROL KINASE PD130307: F20-K137 FGGY family of carbohydrate kinase proteins BL00933: F20-C43, Y54-P64, S159-N178, T212-V248, G414-I429</p>	BLAST-PRODOME BLAST-PRODOME BLAST-PRODOME BLIMPS-BLOCKS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
18					FGY family of carbohydrate kinases signatures prok_carb_kinases.prf: P350-K409 FGY family of carbohydrate kinases FGY: L92-R122, L172-D224, F238-A448 Fgy_Kinases_2: A366-E386	PROFILERSCAN HMMER-PFAM MOTIFS
19	7477204CD1	553	S187 S23 S36 S380 S399 S544 S58 T138 T139 T213 T348 T407 T537 T79 T85	N418 N543	PROTEIN KINASE DOMAIN DM00004 P32298 157-401: F194-G440 RECEPTOR KINASE PD001932: K455-N531 Regulator of G-protein PF00615: F163-K179 V267-I280 Tyrosine kinase catalytic domain signature PR00109: F419-S441, M268-Y281, H306-L324, G352-L362, V372-Y394 GPCR kinase signature PR00717: Y172-Q184, K230-S248, P469-I486, V492-F505, N507-T524 Protein kinases signatures and profile protein_kinase_tyr.prf: R292-K345 Regulator of G protein signaling domain RGS: N55-p78, P162-L176 Eukaryotic protein kinase domain pkinase: F191-F454 Protein_Kinase_Atp: L197-K220 Protein_Kinase_St: I312-L324	BLAST-DOMO BLAST-PRODROM BLIMPS-PFAM BLIMPS-PRINTS BLIMPS-PRINTS PROFILERSCAN HMMER-PFAM HMMER-PFAM MOTIFS MOTIFS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
20	3016969CD1	871	S121 S123 S135 S153 S167 S203 S293 S33 S353 S409 S542 S557 S571 S597 S640 S652 S665 S667 S727 S81 T172 T417 T516 T526 T76 T844	N211	PROTEIN KINASE DOMAIN DM00004 S07571 5152-5396: Q580-P812 Tyrosine PR00109: Y684-I702, T751-E773, I581-A603 Eukaryotic protein kinase domain pkinase: F575-L827 Protein_Kinase_Tyr: I690-I702	BLAST-DOMO BLIMPS-PRINTS HMMER-PFAM MOTIFS
21	063497CD1	765	S162 S181 S259 S286 S291 S410 S431 S437 S472 S479 S495 S531 S539 S544 S550 S569 S576 S597 S639 S646 S661 S676 T172 T319 T365 T474 T478 T50 T543 T622 T623 T684 T714 T716	N219 N289 N588 N618	Eukaryotic protein kinase domain: Y16-L269 Tyrosine kinase catalytic domain signature PR00109:L92-M105, Y129-F147, V238-L260 SNF1RELATED KINASE PD127501:Q346-D579 PD070820:T715-I765, E642-G693, I345-P370 ZK524.4 PROTEIN SNF1RELATED KINASE PD156028:I282-I345 KINASE TRANSFERASE ATP BINDING SERINE/THREONINE PHOSPHORYLATION RECEPTOR TYROSINE TRANSMEMBRANE PD000001:L18-V145, V238-W268, G168-F215 PROTEIN KINASE DOMAIN DM00004 P27448 58-297:K20-L260 DM00004 I48609 55-294:K20-L260 DM00004 Q05512 55-294:K20-L260 DM00004 JC1446 20-261:L18-L260	HMMER_PFAM BLIMPS_PRINTS BLAST_PRODROM BLAST_PRODROM BLAST_PRODROM BLAST_DOMO

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
21					Protein kinases ATP-binding region signature: L22-K45 Serine/Threonine protein kinases active-site signature: V135-F147	MOTIFS
22	1625436CD1	588	S109 S355 S356 S36 S427 S433 S51 S557 S79 T262 T383 T408 T409 T410 T47 T488 T94	N313 N394 N407 N424	Eukaryotic protein kinase domain: Y14-V272 Protein kinases signatures and profile: F85-E167 Tyrosine kinase catalytic domain signature PR00109:HL26-L144 KINASE II CALCIUM/CALMODULIN DEPENDENT SUBUNIT TRANSFERASE SERINE/THREONINE PD004250:E500-Q588 PD001779:R456-V499, V272-S329, T396-A417 PROTEIN KINASE DOMAIN DM00004 P11798 15-261:L16-A263 DM00004 JU0270 16-262:E18-A263 DM00004 A44412 16-262:E18-A263 DM00004 S57347 21-266:L20-T262 Protein kinases ATP-binding region signature: L20-K43 Serine/Threonine protein kinases active-site signature: I132-L144	HMMER_PFAM PROFILES SCAN BLIMPS_PRINTS BLAST_PRODOR
						ELAST_DOMO
						MOTIFS
						MOTIFS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
23	3330646CD1	1798	S74 S92 S1084 S108 S130 S1100 S166 S171 S1205 S200 S204 S1195 S230 S253 S1214 S281 S480 S1230 S503 S508 S1225 S533 S775 S1229 S806 S811 S1272 S817 S825 S1256 S846 S854 S1332 S860 S874 S1337 S909 S914 S1418 S931 S1425 S1429 S1447 S1459 S1491 S1503 S1504 S1541 S1650 S1657 S1660 S1671 S1698 S1717 S1771 T266 T506 T1014 T514 T565 T1036 T581 T729 T1040 T759 T786 T1117 T815 T82 T1189 T871 T916 T1236 T925 T949 T1244 T1424 T1480 T1675 T1765	N142 N1193 N1252 N1293	Eukaryotic protein kinase domain: F512-F785	HMMER_PFAM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosyla- tion Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
23					PDZ domain: P1104-L1191	HMMER_PFAM
					Protein kinases signatures and profile: F579-M659	PROFILES SCAN
					Tyrosine kinase catalytic domain signature PR00109:M589-K602, Y625-I643, V706-D728	BLIMPS_PRINTS
					MICROTUBULE ASSOCIATED TESTIS SPECIFIC SERINE/THREONINE PROTEIN KINASE PD142315:H1313-T1798 PD135564:V61-Y320, L1151-P1363 PD182663:E863-H1139	BLAST_PROD OM
					PROTEIN KINASE SERINE/THREONINE KIN4 MICROTUBULE ASSOCIATED TESTIS SPECIFIC PD041650:K321-D511	BLAST_PROD OM
					PROTEIN KINASE DOMAIN DM00004 A54602 455-712:T514-G772 DM08046 P05986 1-397: S508-K658, V685-E829, D268-P291 DM00004 S42867 75-498: I515-T666, H672-F813 DM00004 S42864 41-325: E513-K658, H672-T773	BLAST_DOMO
					Serine/Threonine protein kinases active- site signature: I631-I643	MOTIFS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
24	3562763CD1	362	S123 S157 S25 S325 S81 T164 T197 T260 T280 T286 T324 T353	N110 N165	transmembrane domain: A263-D283 Eukaryotic protein kinase domain: Y30-L351 Protein kinases signatures and profile: T164-G218 Tyrosine kinase catalytic domain signature PR00109: M143-L156, F178-I196, M326-A348 PROTEIN KINASE DOMAIN DM00004 Q02723 16-259: K111-V215, N232-V304 DM00004 A54602 455-712:N110-L316, I36-I61 DM00004 P23573 10-277: L139-K214, E35-L102, F248-A348 DM00004 A57459 417-662:Y138-S325, E35-L73 Protein kinases ATP-binding region signature: I36-K59 Serine/Threonine protein kinases active-site signature: I184-I196	HMMER HMMER_PFAM PROFILES SCAN BLIMPS_PRINTS BLAST_DOMO MOTIFS MOTIFS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
25	621293CD1	275			Adenylate kinase: L69-P205	HMMER_PFAM
					Adenylate kinase proteins. BL00113:L68-L84, N92-R135, C141-L155	BLIMPS_BLOCKS
					Adenylate kinase signature PR00094:L68-A81, G96-G110, W146-N162	BLIMPS_PRINTS
26	7480774CD1	660	S104 S106 S167 S199 S226 S325 S338 S339 S343 S355 S381 S458 S46 S629 S96 T117 T151 T160 T183 T210 T468 T500 T83 T90 T99	N177	INOSITOL 3 KINASE 1D MYOINOSITOL TRISPHOSPHATE 5 TRISPHOSPHATE IP3K IP3 TRANSFERASE KINASE CALMODULIN BINDING PD010031:Q446-Q659, P377-Q442 CALMODULIN-BINDING DOMAIN DM07435 P42335 210-672:E315-Q659 DM07435 P23677 1-461:G261-Q659	BLAST_PRODOM BLAST_DOMO

Table 4

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment (s)	Sequence Fragments	5' Position	3' Position
27	2011384CB1	822	282-377	6829315H1 (SINTNOR01) g2954208 5545302T6 (TESTNOC01) 674588R6 (CRBLNOT01) 5562195F8 (BRSTDIT01)	44 1 713 517 1	743 282 1376 1256 644
28	2004888CB1	1376	1349-1376, 499-635	3219989H1 (COLNNON03) 2258952T6 (OVRTUT01) FL2258952_g7458755_ 000012_g3766209 7126256H1 (COLNDIY01) g1633937 7677920H1 (NOSETUE01) 2660853T6 (LUNGTUT09) 5216205F6 (BRSTNOT35) 6854507F8 (BRAIFEN08) 55057226H1 5911008F6 (BRAIFEN05) 2074751F6 (ISLTNOT01) 6881535J1 (BRAHTDR03) 70006068D1 70006347D1 7934296H1 (COLNDIS02) 70003021D1 7226035H1 (LUNGTMC01)	3223 2757 33 2527 2718 1 2249 1789 763 354 1299 1626 1 1296 1162 2109 1740 725	3468 3353 2849 3076 3385 601 2831 2681 1471 1145 1988 2118 582 1838 1747 2693 2337 1187
29	2258952CB1	3468	1-983, 1461-1908, 3369-3468			
30	7473244CB1	2831	1-243, 834-1782			
31	1242491CB1	2693	1-317, 2569-2693			

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
31				5755513H1 (LJUNGNOT35)	672	1102
				70004229D1	1874	2338
				55052947H1	1	694
32	2634875CB1	2973	1-1353, 2203- 2560	4009430F6 (MUSCNOT10)	959	1432
				5168601H1 (MUSCDMT01)	1691	1965
				5672440H1 (MUSLTD01)	2213	2414
				6903523H1 (MUSLTD02)	1833	2344
				55052146J1	1475	1654
				6217472F6 (MUSCDIT06)	2263	2973
				3585116F6 (293TF4T01)	623	1126
				GBI.g7242443_000006 .edit	1059	1585
				55052619J1	1	807
				2634875H1 (BONTNOT01)	1521	1764
33	3951059CB1	2066	532-772, 1830- 1886, 1966-2066	6882814J1 (BRAHTDR03)	1489	2066
				55058330J1	396	1316
				FL452484_00001	1	970
				71179403V1	1052	1745
34	7395890CB1	3975	1-326, 3951- 3975, 2980-3355, 3666-3731, 1813- 2074, 1066-1098	6771964H1 (BRAUNOR01)	715	1432
				6770122H1 (BRAUNOR01)	1471	2040
				6771964J1 (BRAUNOR01)	2028	2713
				7393659H1 (BRABDIE02)	186	799
				55052405H1	1	218
				2570554R6 (HIPOAZT01)	2495	3012
				7660364H1 (OVARNOE02)	1861	2459
				FL034583_00001	2778	3584

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
34				7395271H1 (BRABDIE02)	256	896
				6200064H1 (PITUNON01)	2715	3162
				7395911H1 (BRABDIE02)	896	1481
				GNN.g8439948_000007 .edit2.comp	3181	3975
				6873077H1 (BRAGNON02)	1327	1999
35	7475546CB1	1918	1-46, 658-1061	6623984J1 (UTRMTMR02)	655	1287
				7192851H2 (BRATDIC01)	497	1107
				6810083J1 (SKIRNOR01)	1254	1918
				7013748H1 (KIDNNOC01)	1	580
				7190770H1 (BRATDIC01)	216	771
36	7477076CB1	1689	1-66	55051332H1	1	282
				6819441H1 (OVARDIR01)	1077	1689
				7758313J1 (SPINTUE01)	558	922
				GNN:g807680_edit	820	1476
				1874092F6 (LEUKNOT02)	604	1054
37	1874092CB1	1054	1-30	7315561H1 (SYNODIN02)	1	633
				71224917V1	2797	3360
				70858292V1	2345	3032
				8045106H1 (OVARTUE01)	1719	2379
				7617315J1 (KIDNTUE01)	1036	1632
38	4841542CB1	3360	1-172, 2484- 2523, 650-1457, 2247-2417	7609838J1 (KIDCTME01)	783	1346
				70856122V1	2494	3142
				71225608V1	1597	2126
				55053856H1	1	826

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
39	7472695CB1	2240	1-20, 101-131, 704-1001	7191541F6 (BRATDIC01)	1	906
				71872279V1	911	1501
				4211726T8 (BRONDI01)	1466	2181
				71870527V1	1717	2240
				71870095V1	669	1374
				2013786T6 (TESTNOT03)	1551	2217
				1513994T6 (PANCUTUT01)	2768	3340
40	7477966CB1	3340	1-980, 1504- 1710, 3315-3340	6802962H1 (COLEENOR03)	2241	2824
				55052773H1	1376	2254
				1513994F6 (PANCUTUT01)	2155	2776
				55052765H1	894	1745
				7607337J1 (COLRTUE01)	594	1258
				6802518H1 (COLEENOR03)	551	858
				7677920H1 (NOSETUE01)	1	598
				7715351J1 (SINTFEE02)	1	649
				1625532H1 (COLNPOF01)	1779	1993
				7163416F8 (PLACNOR01)	1888	2539
41	7163416CB1	2539	1-228, 913-1225, 1994-2539	7701682J1 (PENHTUE02)	815	1434
				7715351H1 (SINTFEE02)	399	1037
				7077243H1 (BRAUTDR04)	1306	1979
				71982976V1	913	1546
				71983661V1	793	1520
				71986606V1	1494	2168
				55052941J1	1	886
				71983943V1	1551	2193
				71983660V1	1642	2377
42	7472822CB1	2377	2341-2377, 1093- 1463, 1625-2081			

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
43	7477486CB1	2897	2698-2763, 1- 365, 2314-2623, 1516-1614, 2804- 2897	4029722F8 (BRAINOT23)	2042	2584
				6910737R6 (PITUDIR01)	462	1370
				7237528H1 (BRAINOY02)	2348	2897
				7674962H2 (NOSETUE01)	125	589
				71982594V1	1386	1991
				6629715R6 (HEALDIR01)	637	1476
				GNN.g6165121_004.ed it	1	506
				6950253H1 (BRAITDR02)	1480	2176
				6938382F6 (FTUBTUR01)	116	850
				4383108H1 (BRAVUTT02)	1	257
44	3773709CB1	3361	1-168, 1479- 1982, 3336-3361	7365206H1 (OVARDIC01)	2019	2580
				55024481H1 (PKINDNV08)	791	1462
				4119492H1 (BRSTTUT25)	3104	3361
				70783206V1	1969	2579
				3432983T6 (SKINNOT04)	2555	3217
				70782455V1	1361	2005
				70143324V1	2631	3219
				70784860V1	1463	2006
				GNN.g8139716_edit	1	1662
				71873834V1	1555	2122
45	7477204CB1	1662	854-1662, 1-807	5751549F8 (LUNGNOT35)	2153	2740
				7718401J1 (SINTFEE02)	1341	2100
				7354408H1 (HEARNON03)	2779	3225
				71872969V1	1969	2707
				71875134V1	885	1440
46	3016969CB1	3225	1-916, 1154- 1362, 3144-3225			

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
46				3016969T6 (MUSCNOT07)	2532	3211
				6200811F6 (PITUNON01)	808	1403
				55052669H1	1	852
47	063497CB1	4772	1-431, 4420- 4540, 2098-2130, 3522-3599, 2875- 3036	6581829H1 (HEACDIC01)	2823	3464
				7199634H1 (LUNGFER04)	602	1153
				6936880H1 (FTVUTUR01)	3000	3714
				1449223H1 (PLACNOT02)	4029	4248
				4787168H1 (BRATNOT03)	3705	3964
				7714789H1 (SINTFEE02)	1198	1849
				7714789J1 (SINTFEE02)	4189	4772
				063497H1 (PLACNOB01)	1661	1880
				8025257J1 (ENDMUNE01)	1	702
				7381417H1 (ENDMUNE01)	1790	2359
				4351289H1 (CONFMT01)	3884	4222
				5068175H1 (PANCNOT23)	3675	3946
				7380657H1 (ENDMUNE01)	772	1305
				4051307H1 (SINTNOT18)	2689	2972
				7627517J1 (GBLADIE01)	2393	2919
				7629590H1 (GBLADIE01)	1953	2559
48	1625436CB1	1880	948-1167	5772228H1 (BRATNOT20)	844	1420
				72285173V1	673	1148

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
48				7353062H1 (HEARNON03)	1	610
				7154515H1 (BRAMNOA01)	1164	1839
				6764194H1 (BRAUNOR01)	1370	1880
				72284772V1	491	1135
				8178338H2 (EYERNON01)	5053	5722
				7218734H1 (COLNIMC01)	4882	5570
				8013776H1 (HEARNOC04)	4245	4904
				8006864H1 (PENIFEC01)	442	1064
				7711762H2 (TESTTUE02)	688	1292
				55124907H1	1301	2151
49	3330646CB1	5747	1-1738, 2291- 2733, 3677-4763	8009629H1 (NOSEDIC02)	3681	4314
				7054991H1 (BRALNON02)	5099	5747
				55124907J1	1250	2101
				8267426H1 (MLXDUNF03)	2739	3511
				8054655J1 (ESOGTUE01)	2905	3529
				7930953H1 (COLNDIS02)	4339	4966
				7978939H1 (LSUBDMC01)	1	504
				7719236J1 (SINTFEE02)	2085	2746
				60215898V1	2234	2776
				6779321J1 (OVARDIR01)	3439	4230
50	3562763CB1	3418	1564-1627, 1- 376, 975-1073, 3066-3418	55053205H1	523	1210
				7321924H1 (NOSETTUE01)	1843	2392
				7278180H1 (BMARTXE01)	2873	3418

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
50				400518R6	873	1430
				(PITUNOT02)		
				6816641J1	1297	1981
				(ADRETUR01)		
				g2963935	1	383
				55143790J1	2257	3143
51	621293CB1	995	1-372, 410-468	55067380J2	314	579
				55143774J1	2577	3148
				72335268V1	1	508
				71870548V1	477	994
52	7480774CB1	2459	1664-2459, 1-110	71440281V1	685	1345
				71438714V1	652	1226
				7082565H1	1	688
				(STOMTMR02)		
				71432228V1	1798	2459
				71431941V1	1257	1972
				6472388H1	1352	1985
				(PLACFEB01)		

Table 5

Polynucleotide SEQ ID NO:	Incyte Project ID	Representative Library
27	2011384CB1	SINTNOR01
28	2004888CB1	TESTNOT03
29	2258952CB1	COLENOR03
30	7473244CB1	ISLTNOT01
31	1242491CB1	LUNGNOT02
32	2634875CB1	MUSCNOT07
33	3951059CB1	DRGCNOT01
34	7395890CB1	BRADIE02
35	7475546CB1	CORPNOT02
36	7477076CB1	BRATDIC01
37	1874092CB1	LEUKNOT02
38	4841542CB1	KIDNNOT05
39	7472695CB1	TESTNOT03
40	7477966CB1	COLENOR03
41	7163416CB1	ESOGTME01
42	7472822CB1	BRABDIR03
43	7477486CB1	BRAITDR03
44	3773709CB1	SINTNOR01
46	3016969CB1	COLNNOT41
47	063497CB1	ENDMUNE01
48	1625436CB1	BRACNOK02
49	3330646CB1	HNT2AGT01
50	3562763CB1	BRAHNOE01
51	621293CB1	KIDNNOT09
52	7480774CB1	BLADTUT02

Table 6

Library	Vector	Library Description
BLADTUT02	pINCY	Library was constructed using RNA isolated from bladder tumor tissue removed from an 80-year-old Caucasian female during a radical cystectomy and lymph node excision. Pathology indicated grade 3 invasive transitional cell carcinoma. Family history included acute renal failure, osteoarthritis, and atherosclerosis.
BRADIE02	pINCY	This 5' biased random primed library was constructed using RNA isolated from diseased cerebellum tissue removed from the brain of a 57-year-old Caucasian male who died from a cerebrovascular accident. Serologies were negative. Patient history included Huntington's disease, emphysema, and tobacco abuse (3-4 packs per day, for 40 years).
BRABDIR03	pINCY	Library was constructed using RNA isolated from diseased cerebellum tissue removed from the brain of a 57-year-old Caucasian male who died from a cerebrovascular accident. Serologies were negative. Patient history included Huntington's disease, emphysema, and tobacco abuse (3-4 packs per day for 40 years).
BRACNOK02	PSPORT1	This amplified and normalized library was constructed using RNA isolated from posterior cingulate tissue removed from an 85-year-old Caucasian female who died from myocardial infarction and retroperitoneal hemorrhage. Pathology indicated atherosclerosis, moderate to severe, involving the circle of Willis, middle cerebral, basilar and vertebral arteries; infarction, remote, left dentate nucleus; and amyloid plaque deposition consistent with age. There was mild to moderate leptomeningeal fibrosis, especially over the convexity of the frontal lobe. There was mild generalized atrophy involving all lobes. The white matter was mildly thinned. Cortical thickness in the temporal lobes, both maximal and minimal, was slightly reduced. The substantia nigra pars compacta appeared mildly depigmented. Patient history included COPD, hypertension, and recurrent deep venous thrombosis. 6.4 million independent clones from this amplified library were normalized in one round using conditions adapted Soares et al., PNAS (1994) 91:9228-9232 and Bonaldo et al., Genome Research 6 (1996):791.
BRAHNOE01	pINCY	Library was constructed RNA isolated from posterior hippocampus tissue removed from a 45-year-old Caucasian female who died from a dissecting aortic aneurysm and ischemic bowel disease. Pathology indicated mild arteriosclerosis involving the cerebral cortical white matter and basal ganglia. Grossly, there was mild meningeal fibrosis and mild focal atherosclerotic plaque in the middle cerebral artery, as well as vertebral arteries bilaterally. Microscopically, the cerebral hemispheres, brain stem and cerebellum revealed focal areas in the white matter that contain blood vessels that were barrel-shaped, hyalinized, with hemosiderin-laden macrophages in the Virchow-Robin space. In addition, there were scattered neurofibrillary tangles within the basolateral nuclei of the amygdala. Patient

Table 6 (cont.)

Library	Vector	Library Description
BRAITDR03	PCDNA2.1	history included mild atheromatosis of aorta and coronary arteries, bowel and liver infarct due to aneurysm, physiologic fatty liver associated with obesity, mild diffuse emphysema, thrombosis of mesenteric and portal veins, cardiomegaly due to hypertrophy of left ventricle, arterial hypertension, acute pulmonary edema, splenomegaly, obesity (300 lb.), leiomyoma of uterus, sleep apnea, and iron deficiency anemia. This random primed library was constructed using RNA isolated from allocortex, cingulate posterior tissue removed from a 55-year-old Caucasian female who died from cholangiocarcinoma. Pathology indicated mild meningeal fibrosis predominately over the convexities, scattered axonal spheroids in the white matter of the cingulate cortex and the thalamus, and a few scattered neurofibrillary tangles in the entorhinal cortex and the periaqueductal gray region. Pathology for the associated tumor tissue indicated well-differentiated cholangiocarcinoma of the liver with residual or relapsed tumor. Patient history included cholangiocarcinoma, post-operative Budd-Chiari syndrome, biliary ascites, hydrothorax, dehydration, malnutrition, oliguria and acute renal failure. Previous surgeries included cholecystectomy and resection of 85% of the liver.
BRATDIC01	pINCY	This large size-fractionated library was constructed using RNA isolated from diseased brain tissue removed from the left temporal lobe of a 27-year-old Caucasian male during a brain lobectomy. Pathology for the left temporal lobe, including the mesial temporal structures, indicated focal, marked pyramidal cell loss and gliosis in hippocampal sector CA1, consistent with mesial temporal sclerosis. The left frontal lobe showed a focal deep white matter lesion, characterized by marked gliosis, calcifications, and hemosiderin-laden macrophages, consistent with a remote perinatal injury. The frontal lobe tissue also showed mild to moderate generalized gliosis, predominantly subpial and subcortical, consistent with chronic seizure disorder. GFAP was positive for astrocytes. The patient presented with intractable epilepsy, focal epilepsy, hemiplegia, and an unspecified brain injury. Patient history included cerebral palsy, abnormality of gait, depressive disorder, and tobacco abuse in remission. Previous surgeries included tendon transfer. Patient medications included minocycline hydrochloride, Tegretol, phenobarbital, vitamin C, Pepcid, and Pevaryl. Family history included brain cancer in the father.
COLENOR03	PCDNA2.1	Library was constructed using RNA isolated from colon epithelium tissue removed from a 13-year-old Caucasian female who died from a motor vehicle accident.
COLNNOT41	pINCY	Library was constructed using RNA isolated from colon tissue removed from a 37-year-old female during a partial gastrectomy. Pathology indicated a portion

Table 6 (cont.)

Library	Vector	Library Description
		of stomach and jejunum with an intact anastomotic site. The stomach showed a mild chronic gastritis without helicobacter pylori organisms. Normal appearing submucosal and myenteric plexus ganglion cells were noted. The jejunum had no significant abnormality.
CORPNOT02	pINCY	Library was constructed using RNA isolated from diseased corpus callosum tissue removed from the brain of a 74-year-old Caucasian male who died from Alzheimer's disease.
DRGCNOT01	pINCY	Library was constructed using RNA isolated from dorsal root ganglion tissue removed from the cervical spine of a 32-year-old Caucasian male who died from acute pulmonary edema and bronchopneumonia, bilateral pleural and pericardial effusions, and malignant lymphoma (natural killer cell type). Patient history included probable cytomegalovirus, infection, hepatic congestion and steatosis, splenomegaly, hemorrhagic cystitis, thyroid hemorrhage, and Bell's palsy. Surgeries included colonoscopy, large intestine biopsy, adenotonsillectomy, and nasopharyngeal endoscopy and biopsy; treatment included radiation therapy.
ENDMUNE01	pINCY	This 5' biased random primed library was constructed using RNA isolated from untreated umbilical artery endothelial cell tissue removed from a Caucasian male (Clonetics) newborn.
ESOGTME01	PSPORT1	This 5' biased random primed library was constructed using RNA isolated from esophageal tissue removed from a 53-year-old Caucasian male during a partial esophagectomy, proximal gastrectomy, and regional lymph node biopsy. Pathology indicated no significant abnormality in the non-neoplastic esophagus. Pathology for the matched tumor tissue indicated invasive grade 4 (of 4) adenocarcinoma, forming a sessile mass situated in the lower esophagus, 2 cm from the gastroesophageal junction and 7 cm from the proximal margin. The tumor invaded through the muscularis propria into the adventitial soft tissue. Metastatic carcinoma was identified in 2 of 5 paragastric lymph nodes with perinodal extension. The patient presented with dysphagia. Patient history included membranous nephritis, hyperlipidemia, benign hypertension, and anxiety state. Previous surgeries included an adenotonsillectomy, appendectomy, and inguinal hernia repair. The patient was not taking any medications. Family history included atherosclerotic coronary artery disease, alcoholic cirrhosis, alcohol abuse, and an abdominal aortic aneurysm rupture in the father; breast cancer in the mother; a myocardial infarction and atherosclerotic coronary artery disease in the sibling(s); and myocardial infarction and atherosclerotic coronary artery disease in the grandparent(s).
HNT2AGT01	PBLUESCRIPT	Library was constructed at Stratagene (STR937233), using RNA isolated from the

Table 6 (cont.)

Library	Vector	Library Description
		hNT2 cell line derived from a human teratocarcinoma that exhibited properties characteristic of a committed neuronal precursor. Cells were treated with retinoic acid for 5 weeks and with mitotic inhibitors for two weeks and allowed to mature for an additional 4 weeks in conditioned medium.
ISLTNOT01	pINCY	Library was constructed using RNA isolated from a pooled collection of pancreatic islet cells.
KIDNNOT05	PSPORT1	Library was constructed using RNA isolated from the kidney tissue of a 2-day-old Hispanic female, who died from cerebral anoxia. Family history included congenital heart disease.
KIDNNOT09	pINCY	Library was constructed using RNA isolated from the kidney tissue of a Caucasian male fetus, who died at 23 weeks' gestation.
LEUKNOT02	pINCY	Library was constructed using RNA isolated from white blood cells of a 45-year-old female with blood type O+. The donor tested positive for cytomegalovirus (CMV).
LUNGNOT02	PBLUESCRIPT	Library was constructed using RNA isolated from the lung tissue of a 47-year-old Caucasian male, who died of a subarachnoid hemorrhage.
MUSCNOT07	pINCY	Library was constructed using RNA isolated from muscle tissue removed from the forearm of a 38-year-old Caucasian female during a soft tissue excision. Pathology for the associated tumor tissue indicated intramuscular hemangioma. Family history included breast cancer, benign hypertension, cerebrovascular disease, colon cancer, and type II diabetes.
SINTNOR01	PCDNA2.1	This random primed library was constructed using RNA isolated from small intestine tissue removed from a 31-year-old Caucasian female during Roux-en-Y gastric bypass. Patient history included clinical obesity.
TESTNOT03	PBLUESCRIPT	Library was constructed using RNA isolated from testicular tissue removed from a 37-year-old Caucasian male, who died from liver disease. Patient history included cirrhosis, jaundice, and liver failure.

Table 7

Program	Description	Reference	Parameter Threshold
ABIFACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25:3389-3402.	<i>ESTs</i> : Probability value= 1.0E-8 or less <i>Full Length sequences</i> : Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad. Sci. USA 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183:63-98; and Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489.	<i>ESTs</i> : fasta E value=1.06E-6 <i>Assembled ESTs</i> : fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value=1.0E-8 or less <i>Full Length sequences</i> : fastx score=100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff (1991) Nucleic Acids Res. 19:6565-6572; Henikoff, J.G. and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37:417-424.	Probability value= 1.0E-3 or less
HMMER	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM.	Krogh, A. et al. (1994) J. Mol. Biol. 235:1501-1531; Somnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322; Durbin, R. et al. (1998) Our World View, in a Nutshell, Cambridge Univ. Press, pp. 1-350.	<i>PFAM hits</i> : Probability value= 1.0E-3 or less <i>Signal peptide hits</i> : Score= 0 or greater

Table 7 (cont.)

Program	Description	Reference	Parameter Threshold
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, M. et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221.	Normalized quality score> GCG-specified "HIGH" value for that particular Prosite motif. Generally, score=1.4-2.1.
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M.S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies.	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12:431-439.	Score=3.5 or greater
TMAP	A program that uses weight matrices to delineate transmembrane segments on protein sequences and determine orientation.	Persson, B. and P. Argos (1994) J. Mol. Biol. 237:182-192; Persson, B. and P. Argos (1996) Protein Sci. 5:363-371.	
TMHMMER	A program that uses a hidden Markov model (HMM) to delineate transmembrane segments on protein sequences and determine orientation.	Sonnhammer, E.L. et al. (1998) Proc. Sixth Intl. Conf. on Intelligent Systems for Mol. Biol., Glasgow et al., eds., The Am. Assoc. for Artificial Intelligence Press, Menlo Park, CA, pp. 175-182.	
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

What is claimed is:

1. An isolated polypeptide selected from the group consisting of:

a) a polypeptide comprising an amino acid sequence selected from the group consisting of

5 SEQ ID NO:1-26,

b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-26,

c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, and

10 d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26.

2. An isolated polypeptide of claim 1 selected from the group consisting of SEQ ID NO:1-

26.

15

3. An isolated polynucleotide encoding a polypeptide of claim 1.

4. An isolated polynucleotide encoding a polypeptide of claim 2.

20 5. An isolated polynucleotide of claim 4 selected from the group consisting of SEQ ID NO:27-52.

6. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 3.

25

7. A cell transformed with a recombinant polynucleotide of claim 6.

8. A transgenic organism comprising a recombinant polynucleotide of claim 6.

30 9. A method for producing a polypeptide of claim 1, the method comprising:

a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide comprises a promoter sequence operably linked to a polynucleotide encoding the polypeptide of claim 1, and

35 b) recovering the polypeptide so expressed.

10. An isolated antibody which specifically binds to a polypeptide of claim 1.

11. An isolated polynucleotide selected from the group consisting of:

a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting
5 of SEQ ID NO:27-52,

b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:27-52,

c) a polynucleotide complementary to a polynucleotide of a),

d) a polynucleotide complementary to a polynucleotide of b), and

10 e) an RNA equivalent of a)-d).

12. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide of claim 11.

15 13. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:

a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe
20 specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and

b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

25 14. A method of claim 13, wherein the probe comprises at least 60 contiguous nucleotides.

15. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:

a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and

30 b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

16. A composition comprising a polypeptide of claim 1 and a pharmaceutically acceptable excipient.

35

17. A composition of claim 16, wherein the polypeptide has an amino acid sequence selected from the group consisting of SEQ ID NO:1-26.

18. A method for treating a disease or condition associated with decreased expression of functional PKIN, comprising administering to a patient in need of such treatment the composition of claim 16.

19. A method for screening a compound for effectiveness as an agonist of a polypeptide of claim 1, the method comprising:

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting agonist activity in the sample.

20. A composition comprising an agonist compound identified by a method of claim 19 and a pharmaceutically acceptable excipient.

21. A method for treating a disease or condition associated with decreased expression of functional PKIN, comprising administering to a patient in need of such treatment a composition of claim 20.

22. A method for screening a compound for effectiveness as an antagonist of a polypeptide of claim 1, the method comprising:

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting antagonist activity in the sample.

23. A composition comprising an antagonist compound identified by a method of claim 22 and a pharmaceutically acceptable excipient.

24. A method for treating a disease or condition associated with overexpression of functional PKIN, comprising administering to a patient in need of such treatment a composition of claim 23.

25. A method of screening for a compound that specifically binds to the polypeptide of claim 1, said method comprising the steps of:

- a) combining the polypeptide of claim 1 with at least one test compound under suitable conditions, and

b) detecting binding of the polypeptide of claim 1 to the test compound, thereby identifying a compound that specifically binds to the polypeptide of claim 1.

26. A method of screening for a compound that modulates the activity of the polypeptide of claim 1, said method comprising:

- a) combining the polypeptide of claim 1 with at least one test compound under conditions permissive for the activity of the polypeptide of claim 1,
- b) assessing the activity of the polypeptide of claim 1 in the presence of the test compound, and
- c) comparing the activity of the polypeptide of claim 1 in the presence of the test compound with the activity of the polypeptide of claim 1 in the absence of the test compound, wherein a change in the activity of the polypeptide of claim 1 in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide of claim 1.

27. A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 5, the method comprising:

- a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,
- b) detecting altered expression of the target polynucleotide, and
- c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

28. A method for assessing toxicity of a test compound, said method comprising:

- a) treating a biological sample containing nucleic acids with the test compound;
- b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 11 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 11 or fragment thereof;
- c) quantifying the amount of hybridization complex; and
- d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

29. A diagnostic test for a condition or disease associated with the expression of PKIN in a biological sample comprising the steps of:

- 5 a) combining the biological sample with an antibody of claim 10, under conditions suitable for the antibody to bind the polypeptide and form an antibody:polypeptide complex; and
- b) detecting the complex, wherein the presence of the complex correlates with the presence of the polypeptide in the biological sample.

30. The antibody of claim 10, wherein the antibody is:

- 10 a) a chimeric antibody,
- b) a single chain antibody,
- c) a Fab fragment,
- d) a $F(ab')_2$ fragment, or
- e) a humanized antibody.

15 31. A composition comprising an antibody of claim 10 and an acceptable excipient.

32. A method of diagnosing a condition or disease associated with the expression of PKIN in a subject, comprising administering to said subject an effective amount of the composition of claim

20 31.

33. A composition of claim 31, wherein the antibody is labeled.

34. A method of diagnosing a condition or disease associated with the expression of PKIN in a subject, comprising administering to said subject an effective amount of the composition of claim
25 33.

35. A method of preparing a polyclonal antibody with the specificity of the antibody of claim
10 comprising:

- 30 a) immunizing an animal with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, or an immunogenic fragment thereof, under conditions to elicit an antibody response;
- b) isolating antibodies from said animal; and

c) screening the isolated antibodies with the polypeptide, thereby identifying a polyclonal antibody which binds specifically to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26.

5 36. An antibody produced by a method of claim 35.

37. A composition comprising the antibody of claim 36 and a suitable carrier.

10 38. A method of making a monoclonal antibody with the specificity of the antibody of claim 10 comprising:

a) immunizing an animal with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26, or an immunogenic fragment thereof, under conditions to elicit an antibody response;

b) isolating antibody producing cells from the animal;

15 c) fusing the antibody producing cells with immortalized cells to form monoclonal antibody-producing hybridoma cells;

d) culturing the hybridoma cells; and

e) isolating from the culture monoclonal antibody which binds specifically to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26.

20

39. A monoclonal antibody produced by a method of claim 38.

40. A composition comprising the antibody of claim 39 and a suitable carrier.

25 41. The antibody of claim 10, wherein the antibody is produced by screening a Fab expression library.

42. The antibody of claim 10, wherein the antibody is produced by screening a recombinant immunoglobulin library.

30

43. A method for detecting a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26 in a sample, comprising the steps of:

a) incubating the antibody of claim 10 with a sample under conditions to allow specific binding of the antibody and the polypeptide; and

b) detecting specific binding, wherein specific binding indicates the presence of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26 in the sample.

5 44. A method of purifying a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26 from a sample, the method comprising:

a) incubating the antibody of claim 10 with a sample under conditions to allow specific binding of the antibody and the polypeptide; and

10 b) separating the antibody from the sample and obtaining the purified polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-26.

45. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:1.

46. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:2.

15

47. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:3.

48. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:4.

20

49. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:5.

50. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:6.

51. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:7.

25

52. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:8.

53. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:9.

30

54. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:10.

55. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:11.

56. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:12.

57. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:13.

58. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:14.

5 59. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:15.

60. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:16.

61. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:17.

10

62. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:18.

63. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:19.

15

64. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:20.

65. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:21.

66. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:22.

20

67. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:23.

68. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:24.

25

69. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:25.

70. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:26.

71. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID

30 NO:27.

72. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:28.

73. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:29.

74. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:30.

75. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:31.

76. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:32.

77. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:33.

78. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:34.

79. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:35.

80. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:36.

81. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:37.

82. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:38.

83. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:39.

84. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:40.

5 85. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:41.

86. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:42.

10 87. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:43.

15 88. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:44.

89. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:45.

20 90. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:46.

91. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:47.

25 92. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:48.

30 93. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:49.

94. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:50.

95. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:51.

96. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
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<110> INCYTE GENOMICS, INC.
 YUE, Henry
 LAL, Preeti
 BANDMAN, Olga
 BOROWSKY, Mark L.
 AU-YOUNG, Janice
 LU, Yan
 GANDHI, Ameena R.
 TRIBOULEY, Catherine M.
 WALIA, Narinder K.
 YAO, Monique G.
 LU, Dyung Aina M.
 GREENWALD, Sara R.
 RAMKUMAR, Jayalaxmi
 GRIFFIN, Jennifer A.
 KEARNEY, Liam
 BURFORD, Neil
 NGUYEN, Dannel B.
 TANG, Y. Tom
 BAUGHN, Mariah R.
 HE, Ann
 THORNTON, Michael
 HAFALIA, April
 PATTERSON, Chandra
 GURURAJAN, Rajagopal
 LO, Terence P.
 KHAH, Farrah A.
 RECIPON, Shirley A.
 AZIMZAI, Yalda
 POLICKY, Jennifer L.
 DING, Li
 GRETHER, Megan
 ELLIOTT, Vicki S.
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 60/228,056

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Glu	Glu	Trp	Asp	Lys	Asp	Val	Ala	Arg	Lys	Leu	Gly	Ser	Thr	Thr
				455					460					465
Val	Gly	Ser	Lys	Ser	Glu	Met	Thr	Ala	Ser	Pro	Leu	Val	Gly	Pro
				470					475					480
Glu	Arg	Lys	Lys	Ser	Ser	Thr	Ile	Pro	Ser	Asn	Asn	Val	Tyr	Ser
				485					490					495
Gly	Gly	Ser	Met	Ala	Arg	Arg	Asn	Thr	Tyr	Val	Cys	Glu	Arg	Thr
				500					505					510
Thr	Asp	Arg	Tyr	Val	Ala	Leu	Gln	Asn	Gly	Lys	Asp	Ser	Ser	Leu
				515					520					525
Thr	Glu	Met	Ser	Val	Ser	Ser	Ile	Ser	Ser	Ala	Gly	Ser	Ser	Val
				530					535					540
Ala	Ser	Ala	Val	Pro	Ser	Ala	Arg	Pro	Arg	His	Gln	Lys	Ser	Met
				545					550					555
Ser	Thr	Ser	Gly	His	Pro	Ile	Lys	Val	Thr	Leu	Pro	Thr	Ile	Lys
				560					565					570
Asp	Gly	Ser	Glu	Ala	Tyr	Arg	Pro	Gly	Thr	Thr	Gln	Arg	Val	Pro
				575					580					585
Ala	Ala	Ser	Pro	Ser	Ala	His	Ser	Ile	Ser	Thr	Ala	Thr	Pro	Asp
				590					595					600
Arg	Thr	Arg	Phe	Pro	Arg	Gly	Ser	Ser	Ser	Arg	Ser	Thr	Phe	His
				605					610					615
Gly	Glu	Gln	Leu	Arg	Glu	Arg	Arg	Ser	Val	Ala	Tyr	Asn	Gly	Pro
				620					625					630
Pro	Ala	Ser	Pro	Ser	His	Glu	Thr	Gly	Ala	Phe	Ala	His	Ala	Arg
				635					640					645
Arg	Gly	Thr	Ser	Thr	Gly	Ile	Ile	Ser	Lys	Ile	Thr	Ser	Lys	Phe
				650					655					660
Val	Arg	Arg	Asp	Pro	Ser	Glu	Gly	Glu	Ala	Ser	Gly	Arg	Thr	Asp
				665					670					675
Thr	Ser	Arg	Ser	Thr	Ser	Gly	Glu	Pro	Lys	Glu	Arg	Asp	Lys	Glu
				680					685					690
Glu	Gly	Lys	Asp	Ser	Lys	Pro	Arg	Ser	Leu	Arg	Phe	Thr	Trp	Ser
				695					700					705
Met	Lys	Thr	Thr	Ser	Ser	Met	Asp	Pro	Asn	Asp	Met	Met	Arg	Glu
				710					715					720
Ile	Arg	Lys	Val	Leu	Asp	Ala	Asn	Asn	Cys	Asp	Tyr	Glu	Gln	Lys

				725						730				735
Glu	Arg	Phe	Leu	Leu	Phe	Cys	Val	His	Gly	Asp	Ala	Arg	Gln	Asp
				740						745				750
Ser	Leu	Val	Gln	Trp	Glu	Met	Glu	Val	Cys	Lys	Leu	Pro	Arg	Leu
				755						760				765
Ser	Leu	Asn	Gly	Val	Arg	Phe	Lys	Arg	Ile	Ser	Gly	Thr	Ser	Ile
				770						775				780
Ala	Phe	Lys	Asn	Ile	Ala	Ser	Lys	Ile	Ala	Asn	Glu	Leu	Lys	Leu
				785						790				795

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 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1242491CD1

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Met	Met	Ser	Trp	Asn	Leu	Asn	Lys	Leu	Gln	Ser	Phe	Leu	Leu	Gly
1				5					10					15
Asp	Gly	Ser	Phe	Gly	Ser	Val	Tyr	Arg	Ala	Ala	Tyr	Glu	Gly	Glu
				20					25					30
Glu	Val	Ala	Val	Lys	Ile	Phe	Asn	Lys	His	Thr	Ser	Leu	Arg	Leu
				35					40					45
Leu	Arg	Gln	Glu	Leu	Val	Val	Leu	Cys	His	Leu	His	His	Pro	Ser
				50					55					60
Leu	Ile	Ser	Leu	Leu	Ala	Ala	Gly	Ile	Arg	Pro	Arg	Met	Leu	Val
				65					70					75
Met	Glu	Leu	Ala	Ser	Lys	Gly	Ser	Leu	Asp	Arg	Leu	Leu	Gln	Gln
				80					85					90
Asp	Lys	Ala	Ser	Leu	Thr	Arg	Thr	Leu	Gln	His	Arg	Ile	Ala	Leu
				95					100					105
His	Val	Ala	Asp	Gly	Leu	Arg	Tyr	Leu	His	Ser	Ala	Met	Ile	Ile
				110					115					120
Tyr	Arg	Asp	Leu	Lys	Pro	His	Asn	Val	Leu	Leu	Phe	Thr	Leu	Tyr
				125					130					135
Pro	Asn	Ala	Ala	Ile	Ile	Ala	Lys	Ile	Ala	Asp	Tyr	Gly	Ile	Ala
				140					145					150
Gln	Tyr	Cys	Cys	Arg	Met	Gly	Ile	Lys	Thr	Ser	Glu	Gly	Thr	Pro
				155					160					165
Gly	Phe	Arg	Ala	Pro	Glu	Val	Ala	Arg	Gly	Asn	Val	Ile	Tyr	Asn
				170					175					180
Gln	Gln	Ala	Asp	Val	Tyr	Ser	Phe	Gly	Leu	Leu	Leu	Tyr	Asp	Ile
				185					190					195
Leu	Thr	Thr	Gly	Gly	Arg	Ile	Val	Glu	Gly	Leu	Lys	Phe	Pro	Asn
				200					205					210
Glu	Phe	Asp	Glu	Leu	Glu	Ile	Gln	Gly	Lys	Leu	Pro	Asp	Pro	Val
				215					220					225
Lys	Glu	Tyr	Gly	Cys	Ala	Pro	Trp	Pro	Met	Val	Glu	Lys	Leu	Ile
				230					235					240
Lys	Gln	Cys	Leu	Lys	Glu	Asn	Pro	Gln	Glu	Arg	Pro	Thr	Ser	Ala
				245					250					255
Gln	Val	Phe	Asp	Ile	Leu	Asn	Ser	Ala	Glu	Leu	Val	Cys	Leu	Thr
				260					265					270
Arg	Arg	Ile	Leu	Leu	Pro	Lys	Asn	Val	Ile	Val	Glu	Cys	Met	Val
				275					280					285
Ala	Thr	His	His	Asn	Ser	Arg	Asn	Ala	Ser	Ile	Trp	Leu	Gly	Cys
				290					295					300
Gly	His	Thr	Asp	Arg	Gly	Gln	Leu	Ser	Phe	Leu	Asp	Leu	Asn	Thr
				305					310					315
Glu	Gly	Tyr	Thr	Ser	Glu	Glu	Val	Ala	Asp	Ser	Arg	Ile	Leu	Cys
				320					325					330
Leu	Ala	Leu	Val	His	Leu	Pro	Val	Glu	Lys	Glu	Ser	Trp	Ile	Val
				335					340					345

Ser	Gly	Thr	Gln	Ser	Gly	Thr	Leu	Leu	Val	Ile	Asn	Thr	Glu	Asp
				350					355					360
Gly	Lys	Lys	Arg	His	Thr	Leu	Glu	Lys	Met	Thr	Asp	Ser	Val	Thr
				365					370					375
Cys	Leu	Tyr	Cys	Asn	Ser	Phe	Ser	Lys	Gln	Ser	Lys	Gln	Lys	Asn
				380					385					390
Phe	Leu	Leu	Val	Gly	Thr	Ala	Asp	Gly	Lys	Leu	Ala	Ile	Phe	Glu
				395					400					405
Asp	Lys	Thr	Val	Lys	Leu	Lys	Gly	Ala	Ala	Pro	Leu	Lys	Ile	Leu
				410					415					420
Asn	Ile	Gly	Asn	Val	Ser	Thr	Pro	Leu	Met	Cys	Leu	Ser	Glu	Ser
				425					430					435
Thr	Asn	Ser	Thr	Glu	Arg	Asn	Val	Met	Trp	Gly	Gly	Cys	Gly	Thr
				440					445					450
Lys	Ile	Phe	Ser	Phe	Ser	Asn	Asp	Phe	Thr	Ile	Gln	Lys	Leu	Ile
				455					460					465
Glu	Thr	Arg	Thr	Ser	Gln	Leu	Phe	Ser	Tyr	Ala	Ala	Phe	Ser	Asp
				470					475					480
Ser	Asn	Ile	Ile	Thr	Val	Val	Val	Asp	Thr	Ala	Leu	Tyr	Ile	Ala
				485					490					495
Lys	Gln	Asn	Ser	Pro	Val	Val	Glu	Val	Trp	Asp	Lys	Lys	Thr	Glu
				500					505					510
Lys	Leu	Cys	Gly	Leu	Ile	Asp	Cys	Val	His	Phe	Leu	Arg	Glu	Val
				515					520					525
Thr	Val	Lys	Glu	Asn	Lys	Glu	Ser	Lys	His	Lys	Met	Ser	Tyr	Ser
				530					535					540
Gly	Arg	Val	Lys	Thr	Leu	Cys	Leu	Gln	Lys	Asn	Thr	Ala	Leu	Trp
				545					550					555
Ile	Gly	Thr	Gly	Gly	Gly	His	Ile	Leu	Leu	Leu	Asp	Leu	Ser	Thr
				560					565					570
Arg	Arg	Leu	Ile	Arg	Val	Ile	Tyr	Asn	Phe	Cys	Asn	Ser	Val	Arg
				575					580					585
Val	Met	Met	Thr	Ala	Gln	Leu	Gly	Ser	Leu	Lys	Asn	Val	Met	Leu
				590					595					600
Val	Leu	Gly	Tyr	Asn	Arg	Lys	Asn	Thr	Glu	Gly	Thr	Gln	Lys	Gln
				605					610					615
Lys	Glu	Ile	Gln	Ser	Cys	Leu	Thr	Val	Trp	Asp	Ile	Asn	Leu	Pro
				620					625					630
His	Glu	Val	Gln	Asn	Leu	Glu	Lys	His	Ile	Glu	Val	Arg	Lys	Glu
				635					640					645
Leu	Ala	Glu	Lys	Met	Arg	Arg	Thr	Ser	Val	Glu				
				650					655					

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 <213> Homo sapiens

<220>
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Ser	Thr	Asp	Lys	Ala	Pro	Lys	Gly	Pro	Thr	Gly	Glu	Arg	Pro	Leu
				20					25					30
Ala	Ala	Gly	Lys	Asp	Pro	Gly	Pro	Pro	Asp	Pro	Lys	Lys	Ala	Pro
				35					40					45
Asp	Pro	Pro	Thr	Leu	Lys	Lys	Asp	Ala	Lys	Ala	Pro	Ala	Ser	Glu
				50					55					60
Lys	Gly	Asp	Gly	Thr	Leu	Ala	Gln	Pro	Ser	Thr	Ser	Ser	Gln	Gly
				65					70					75
Pro	Lys	Gly	Glu	Gly	Asp	Arg	Gly	Gly	Gly	Pro	Ala	Glu	Gly	Ser
				80					85					90
Ala	Gly	Pro	Pro	Ala	Ala	Leu	Pro	Gln	Gln	Thr	Ala	Thr	Pro	Glu
				95					100					105

Thr	Ser	Val	Lys	Lys	Pro	Lys	Ala	Glu	Gln	Gly	Ala	Ser	Gly	Ser
				110					115					120
Gln	Asp	Pro	Gly	Lys	Pro	Arg	Val	Gly	Lys	Lys	Ala	Ala	Glu	Gly
				125					130					135
Gln	Ala	Ala	Ala	Arg	Arg	Gly	Ser	Pro	Ala	Phe	Leu	His	Ser	Pro
				140					145					150
Ser	Cys	Pro	Ala	Ile	Ile	Ser	Ser	Ser	Glu	Lys	Leu	Leu	Ala	Lys
				155					160					165
Lys	Pro	Pro	Ser	Glu	Ala	Ser	Glu	Leu	Thr	Phe	Glu	Gly	Val	Pro
				170					175					180
Met	Thr	His	Ser	Pro	Thr	Asp	Pro	Arg	Pro	Ala	Lys	Ala	Glu	Glu
				185					190					195
Gly	Lys	Asn	Ile	Leu	Ala	Glu	Ser	Gln	Lys	Glu	Val	Gly	Glu	Lys
				200					205					210
Thr	Pro	Gly	Gln	Ala	Gly	Gln	Ala	Lys	Met	Gln	Gly	Asp	Thr	Ser
				215					220					225
Arg	Gly	Ile	Glu	Phe	Gln	Ala	Val	Pro	Ser	Glu	Lys	Ser	Glu	Val
				230					235					240
Gly	Gln	Ala	Leu	Cys	Leu	Thr	Ala	Arg	Glu	Glu	Asp	Cys	Phe	Gln
				245					250					255
Ile	Leu	Asp	Asp	Cys	Pro	Pro	Pro	Pro	Ala	Pro	Phe	Pro	His	Arg
				260					265					270
Met	Val	Glu	Leu	Arg	Thr	Gly	Asn	Val	Ser	Ser	Glu	Phe	Ser	Met
				275					280					285
Asn	Ser	Lys	Glu	Ala	Leu	Gly	Gly	Gly	Lys	Phe	Gly	Ala	Val	Cys
				290					295					300
Thr	Cys	Met	Glu	Lys	Ala	Thr	Gly	Leu	Lys	Leu	Ala	Ala	Lys	Val
				305					310					315
Ile	Lys	Lys	Gln	Thr	Pro	Lys	Asp	Lys	Glu	Met	Val	Leu	Leu	Glu
				320					325					330
Ile	Glu	Val	Met	Asn	Gln	Leu	Asn	His	Arg	Asn	Leu	Ile	Gln	Leu
				335					340					345
Tyr	Ala	Ala	Ile	Glu	Thr	Pro	His	Glu	Ile	Val	Leu	Phe	Met	Glu
				350					355					360
Tyr	Ile	Glu	Gly	Gly	Glu	Leu	Phe	Glu	Arg	Ile	Val	Asp	Glu	Asp
				365					370					375
Tyr	His	Leu	Thr	Glu	Val	Asp	Thr	Met	Val	Phe	Val	Arg	Gln	Ile
				380					385					390
Cys	Asp	Gly	Ile	Leu	Phe	Ser	Val	Leu	Glu	Arg	Val	Leu	His	Leu
				395					400					405
Asp	Leu	Lys	Pro	Glu	Asn	Ile	Leu	Cys	Val	Asn	Thr	Thr	Gly	His
				410					415					420
Leu	Val	Lys	Ile	Ile	Asp	Phe	Gly	Leu	Ala	Arg	Arg	Tyr	Asn	Pro
				425					430					435
Asn	Glu	Lys	Leu	Lys	Val	Asn	Phe	Gly	Thr	Pro	Glu	Phe	Leu	Ser
				440					445					450
Pro	Glu	Val	Val	Lys	Gly	Asp	Gln	Ile	Ser	Asp	Lys	Thr	Asp	Met
				455					460					465
Trp	Ser	Met	Gly	Val	Ile	Thr	Tyr	Met	Leu	Leu	Ser	Gly	Leu	Ser
				470					475					480
Pro	Phe	Leu	Gly	Asp	Asp	Asp	Thr	Glu	Thr	Leu	Asn	Asn	Val	Leu
				485					490					495
Ser	Gly	Asn	Trp	Tyr	Phe	Asp	Glu	Glu	Thr	Phe	Glu	Ala	Val	Ser
				500					505					510
Asp	Glu	Ala	Lys	Asp	Phe	Val	Ser	Asn	Leu	Ile	Val	Lys	Asp	Gln
				515					520					525
Arg	Ala	Arg	Met	Asn	Ala	Ala	Gln	Cys	Leu	Ala	His	Pro	Trp	Leu
				530					535					540
Asn	Asn	Leu	Ala	Glu	Lys	Ala	Lys	Arg	Cys	Asn	Arg	Arg	Leu	Lys
				545					550					555
Ser	Gln	Ile	Leu	Leu	Lys	Lys	Tyr	Leu	Met	Lys	Arg	Arg	Trp	Lys
				560					565					570
Lys	Asn	Phe	Ile	Ala	Val	Ser	Ala	Ala	Asn	Arg	Phe	Lys	Lys	Ile
				575					580					585
Ser	Ser	Ser	Gly	Ala	Leu	Met	Ala	Leu	Gly	Val				
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 Ala Ala Glu Pro Ile Ala Ser Arg Ala Ser Arg Leu Asn Leu Phe
 20 25 30
 Phe Gln Gly Lys Pro Pro Phe Met Thr Gln Gln Gln Met Ser Pro
 35 40 45
 Leu Ser Arg Glu Gly Ile Leu Asp Ala Leu Phe Val Leu Phe Glu
 50 55 60
 Glu Cys Ser Gln Pro Ala Leu Met Lys Ile Lys His Val Ser Asn
 65 70 75
 Phe Val Arg Lys Tyr Ser Asp Thr Ile Ala Glu Leu Gln Glu Leu
 80 85 90
 Gln Pro Ser Ala Lys Asp Phe Glu Val Arg Ser Leu Val Gly Cys
 95 100 105
 Gly His Phe Ala Glu Val Gln Val Val Arg Glu Lys Ala Thr Gly
 110 115 120
 Asp Ile Tyr Ala Met Lys Val Met Lys Lys Lys Ala Leu Leu Ala
 125 130 135
 Gln Glu Gln Val Ser Phe Phe Glu Glu Arg Asn Ile Leu Ser
 140 145 150
 Arg Ser Thr Ser Pro Trp Ile Pro Gln Leu Gln Tyr Ala Phe Gln
 155 160 165
 Asp Lys Asn His Leu Tyr Leu Val Met Glu Tyr Gln Pro Gly Gly
 170 175 180
 Asp Leu Leu Ser Leu Leu Asn Arg Tyr Glu Asp Gln Leu Asp Glu
 185 190 195
 Asn Leu Ile Gln Phe Tyr Leu Ala Glu Leu Ile Leu Ala Val His
 200 205 210
 Ser Val His Leu Met Gly Tyr Val His Arg Asp Ile Lys Pro Glu
 215 220 225
 Asn Ile Leu Val Asp Arg Thr Gly His Ile Lys Leu Val Asp Phe
 230 235 240
 Gly Ser Ala Ala Lys Met Asn Ser Asn Lys Met Val Asn Ala Lys
 245 250 255
 Leu Pro Ile Gly Thr Pro Asp Tyr Met Ala Pro Glu Val Leu Thr
 260 265 270
 Val Met Asn Gly Asp Gly Lys Gly Thr Tyr Arg Leu Asp Cys Asp
 275 280 285
 Trp Trp Ser Val Gly Val Ile Ala Tyr Glu Met Ile Tyr Gly Arg
 290 295 300
 Ser Pro Phe Ala Glu Gly Thr Ser Ala Arg Thr Phe Asn Asn Ile
 305 310 315
 Met Asn Phe Gln Arg Phe Leu Lys Phe Pro Asp Asp Pro Lys Val
 320 325 330
 Ser Ser Asp Phe Leu Asp Leu Ile Gln Ser Leu Leu Cys Gly Gln
 335 340 345
 Lys Glu Arg Leu Lys Phe Glu Gly Leu Cys Cys His Pro Phe Phe
 350 355 360
 Ser Lys Ile Asp Trp Asn Asn Ile Arg Asn Ser Pro Pro Pro Phe
 365 370 375
 Val Pro Thr Leu Lys Ser Asp Asp Asp Thr Ser Asn Phe Asp Glu
 380 385 390
 Pro Glu Lys Asn Ser Trp Val Ser Ser Ser Pro Cys Gln Leu Ser
 395 400 405
 Pro Ser Gly Phe Ser Gly Glu Glu Leu Pro Phe Val Gly Phe Ser
 410 415 420
 Tyr Ser Lys Ala Leu Gly Ile Leu Gly Arg Ser Glu Ser Val Val

	425		430		435
Ser Gly Leu Asp	Ser Pro Ala Lys Thr	Ser Ser Met Glu Lys	Lys		
	440		445		450
Leu Leu Ile Lys	Ser Lys Glu Leu Gln	Asp Ser Gln Asp Lys	Cys		
	455		460		465
His Lys Val Phe	Ile Ser Ala Ala Gly	Leu Leu Pro Cys Ser	Arg		
	470		475		480
Ile Leu Pro Ser	Val Tyr Ala Lys Gly	Ser Ala Arg Gly Arg	Cys		
	485		490		495
Trp Leu					

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Ser Pro His Thr Leu	Gln Ser Ser Ala Phe	Cys Ser Val Lys Lys
20	25	30
Leu Lys Ile Glu Pro	Ser Ser Asn Trp Asp	Met Thr Gly Tyr Gly
35	40	45
Ser His Ser Lys Val	Tyr Ser Gln Ser Lys	Asn Ile Pro Leu Ser
50	55	60
Gln Pro Ala Thr Thr	Thr Val Ser Thr Ser	Leu Pro Val Pro Asn
65	70	75
Pro Ser Leu Pro Tyr	Glu Gln Thr Ile Val	Phe Pro Gly Ser Thr
80	85	90
Gly His Ile Val Val	Thr Ser Ala Ser Ser	Thr Ser Val Thr Gly
95	100	105
Gln Val Leu Gly Gly	Pro His Asn Leu Met	Arg Arg Ser Thr Val
110	115	120
Ser Leu Leu Asp Thr	Tyr Gln Lys Cys Gly	Leu Lys Arg Lys Ser
125	130	135
Glu Glu Ile Glu Asn	Thr Ser Ser Val Gln	Ile Ile Glu Glu His
140	145	150
Pro Pro Met Ile Gln	Asn Asn Ala Ser Gly	Ala Thr Val Ala Thr
155	160	165
Ala Thr Thr Ser Thr	Ala Thr Ser Lys Asn	Ser Gly Ser Asn Ser
170	175	180
Glu Gly Asp Tyr Gln	Leu Val Gln His Glu	Val Leu Cys Ser Met
185	190	195
Thr Asn Thr Tyr Glu	Val Leu Glu Phe Leu	Gly Arg Gly Thr Phe
200	205	210
Gly Gln Val Val Lys	Cys Trp Lys Arg Gly	Thr Asn Glu Ile Val
215	220	225
Ala Ile Lys Ile Leu	Lys Asn His Pro Ser	Tyr Ala Arg Gln Gly
230	235	240
Gln Ile Glu Val Ser	Ile Leu Ala Arg Leu	Ser Thr Glu Ser Ala
245	250	255
Asp Asp Tyr Asn Phe	Val Arg Ala Tyr Glu	Cys Phe Gln His Lys
260	265	270
Asn His Thr Cys Leu	Val Phe Glu Met Leu	Glu Gln Asn Leu Tyr
275	280	285
Asp Phe Leu Lys Gln	Asn Lys Phe Ser Pro	Leu Pro Leu Lys Tyr
290	295	300
Ile Arg Pro Val Leu	Gln Gln Val Ala Thr	Ala Leu Met Lys Leu
305	310	315
Lys Ser Leu Gly Leu	Ile His Ala Asp Leu	Lys Pro Glu Asn Ile
320	325	330
Met Leu Val Asp Pro	Ser Arg Gln Pro Tyr	Arg Val Lys Val Ile

Asp Phe Gly Ser	335	Ala Ser His Val Ser	340	Lys Ala Val Cys Ser	345
	350		355		360
Tyr Leu Gln Ser	365	Arg Tyr Tyr Arg Ala	370	Glu Ile Ile Leu	375
Leu Pro Phe Cys	380	Glu Ala Ile Asp Met	385	Trp Ser Leu Gly Cys	390
Ile Ala Glu Leu	395	Phe Leu Gly Trp Pro	400	Leu Tyr Pro Gly Ala	405
Glu Tyr Asp Gln	410	Ile Arg Tyr Ile Ser	415	Gln Thr Gln Gly Leu	420
Ala Glu Tyr Leu	425	Leu Ser Ala Gly Thr	430	Lys Thr Thr Arg Phe	435
Asn Arg Asp Thr	440	Asp Ser Pro Tyr Pro	445	Leu Trp Arg Leu Lys	450
Pro Asp Asp His	455	Glu Ala Glu Thr Gly	460	Ile Lys Ser Lys Glu	465
Arg Lys Tyr Ile	470	Phe Asn Cys Leu Asp	475	Asp Met Ala Gln Val	480
Met Thr Thr Asp	485	Leu Glu Gly Ser Asp	490	Met Leu Val Glu Lys	495
Asp Arg Arg Glu	500	Phe Ile Asp Leu Leu	505	Lys Lys Met Leu Thr	510
Asp Ala Asp Lys	515	Arg Ile Thr Pro Ile	520	Glu Thr Leu Asn His	525
Phe Val Thr Met	530	Thr His Leu Leu Asp	535	Phe Pro His Ser Thr	540
Val Lys Ser Cys	545	Phe Gln Asn Met Glu	550	Ile Cys Lys Arg Arg	555
Asn Met Tyr Asp	560	Thr Val Asn Gln Ser	565	Lys Thr Pro Phe Ile	570
His Val Ala Pro	575	Ser Thr Ser Thr Asn	580	Leu Thr Met Thr Phe	585
Asn Gln Leu Thr	590	Thr Val His Asn Gln	595	Pro Ser Ala Ala Ser	600
Ala Ala Val Ala	605	Gln Arg Ser Met Pro	610	Leu Gln Thr Gly Thr	615
Gln Ile Cys Ala	620	Arg Pro Asp Pro Phe	625	Gln Gln Ala Leu Ile	630
Cys Pro Pro Gly	635	Phe Gln Gly Leu Gln	640	Ala Ser Pro Ser Lys	645
Ala Gly Tyr Ser	650	Val Arg Met Glu Asn	655	Ala Val Pro Ile Val	660
Gln Ala Pro Gly	665	Ala Gln Pro Leu Gln	670	Ile Gln Pro Gly Leu	675
Ala Gln Gln Ala	680	Trp Pro Ser Gly Thr	685	Gln Gln Ile Leu Leu	690
Pro Ala Trp Gln	695	Gln Leu Thr Gly Val	700	Ala Thr His Thr Ser	705
Gln His Ala Thr	710	Val Ile Pro Glu Thr	715	Met Ala Gly Thr Gln	720
Leu Ala Asp Trp	725	Arg Asn Thr His Ala	730	His Gly Ser His Tyr	735
Pro Ile Met Gln	740	Gln Pro Ala Leu Leu	745	Thr Gly His Val Thr	750
Pro Ala Ala Gln	755	Pro Leu Asn Val Gly	760	Val Ala His Val Met	765
Gln Gln Pro Thr	770	Ser Thr Thr Ser Ser	775	Arg Lys Ser Lys Gln	780
Gln Ser Ser Val	785	Arg Asn Val Ser Thr	790	Cys Glu Val Ser Ser	795
Gln Ala Ile Ser	800	Ser Pro Gln Arg Ser	805	Lys Arg Val Lys Glu	810
Thr Pro Pro Arg	815	Cys Ala Met Val His	820	Ser Ser Pro Ala Cys	825
Thr Ser Val Thr	830	Cys Gly Trp Gly Asp	835	Val Ala Ser Ser Thr	840

Arg	Glu	Arg	Gln	Arg	Gln	Thr	Ile	Val	Ile	Pro	Asp	Thr	Pro	Ser
				845					850					855
Pro	Thr	Val	Ser	Val	Ile	Thr	Ile	Ser	Ser	Asp	Thr	Asp	Glu	Glu
				860					865					870
Glu	Glu	Gln	Lys	His	Ala	Pro	Thr	Ser	Thr	Val	Ser	Lys	Gln	Arg
				875					880					885
Lys	Asn	Val	Ile	Ser	Cys	Val	Thr	Val	His	Asp	Ser	Pro	Tyr	Ser
				890					895					900
Asp	Ser	Ser	Ser	Asn	Thr	Ser	Pro	Tyr	Ser	Val	Gln	Gln	Arg	Ala
				905					910					915
Gly	His	Asn	Asn	Ala	Asn	Ala	Phe	Asp	Thr	Lys	Gly	Ser	Leu	Glu
				920					925					930
Asn	His	Cys	Thr	Gly	Asn	Pro	Arg	Thr	Ile	Ile	Val	Pro	Pro	Leu
				935					940					945
Lys	Thr	Gln	Ala	Ser	Glu	Val	Leu	Val	Glu	Cys	Asp	Ser	Leu	Val
				950					955					960
Pro	Val	Asn	Thr	Ser	His	His	Ser	Ser	Ser	Tyr	Lys	Ser	Lys	Ser
				965					970					975
Ser	Ser	Asn	Val	Thr	Ser	Thr	Ser	Gly	His	Ser	Ser	Gly	Ser	Ser
				980					985					990
Ser	Gly	Ala	Ile	Thr	Tyr	Arg	Gln	Gln	Arg	Pro	Gly	Pro	His	Phe
				995					1000					1005
Gln	Gln	Gln	Gln	Pro	Leu	Asn	Leu	Ser	Gln	Ala	Gln	Gln	His	Ile
				1010					1015					1020
Thr	Thr	Asp	Arg	Thr	Gly	Ser	His	Arg	Arg	Gln	Gln	Ala	Tyr	Ile
				1025					1030					1035
Thr	Pro	Thr	Met	Ala	Gln	Ala	Pro	Tyr	Ser	Phe	Pro	His	Asn	Ser
				1040					1045					1050
Pro	Ser	His	Gly	Thr	Val	His	Pro	His	Leu	Ala	Ala	Ala	Ala	Ala
				1055					1060					1065
Ala	Ala	His	Leu	Pro	Thr	Gln	Pro	His	Leu	Tyr	Thr	Tyr	Thr	Ala
				1070					1075					1080
Pro	Ala	Ala	Leu	Gly	Ser	Thr	Gly	Thr	Val	Ala	His	Leu	Val	Ala
				1085					1090					1095
Ser	Gln	Gly	Ser	Ala	Arg	His	Thr	Val	Gln	His	Thr	Ala	Tyr	Pro
				1100					1105					1110
Ala	Ser	Ile	Val	His	Gln	Val	Pro	Val	Ser	Met	Gly	Pro	Arg	Val
				1115					1120					1125
Leu	Pro	Ser	Pro	Thr	Ile	His	Pro	Ser	Gln	Tyr	Pro	Ala	Gln	Phe
				1130					1135					1140
Ala	His	Gln	Thr	Tyr	Ile	Ser	Ala	Ser	Pro	Ala	Ser	Thr	Val	Tyr
				1145					1150					1155
Thr	Gly	Tyr	Pro	Leu	Ser	Pro	Ala	Lys	Val	Asn	Gln	Tyr	Pro	Tyr
				1160					1165					1170
Ile														

<210> 9

<211> 470

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7475546CD1

<400> 9

Met	Ala	Gly	Pro	Gly	Trp	Gly	Pro	Pro	Arg	Leu	Asp	Gly	Phe	Ile
1				5					10					15
Leu	Thr	Glu	Arg	Leu	Gly	Ser	Gly	Thr	Tyr	Ala	Thr	Val	Tyr	Lys
				20					25					30
Ala	Tyr	Ala	Lys	Lys	Asp	Thr	Arg	Glu	Val	Val	Ala	Ile	Lys	Cys
				35					40					45
Val	Ala	Lys	Lys	Ser	Leu	Asn	Lys	Ala	Ser	Val	Glu	Asn	Leu	Leu
				50					55					60
Thr	Glu	Ile	Glu	Ile	Leu	Lys	Gly	Ile	Arg	His	Pro	His	Ile	Val
				65					70					75

Gln	Leu	Lys	Asp	Phe	Gln	Trp	Asp	Ser	Asp	Asn	Ile	Tyr	Leu	Ile
				80					85					90
Met	Glu	Phe	Cys	Ala	Gly	Gly	Asp	Leu	Ser	Arg	Phe	Ile	His	Thr
				95					100					105
Arg	Arg	Ile	Leu	Pro	Glu	Lys	Val	Ala	Arg	Val	Phe	Met	Gln	Gln
				110					115					120
Leu	Ala	Ser	Ala	Leu	Gln	Phe	Leu	His	Glu	Arg	Asn	Ile	Ser	His
				125					130					135
Leu	Asp	Leu	Lys	Pro	Gln	Asn	Ile	Leu	Leu	Ser	Ser	Leu	Glu	Lys
				140					145					150
Pro	His	Leu	Lys	Leu	Ala	Asp	Phe	Gly	Phe	Ala	Gln	His	Met	Ser
				155					160					165
Pro	Trp	Asp	Glu	Lys	His	Val	Leu	Arg	Gly	Ser	Pro	Leu	Tyr	Met
				170					175					180
Ala	Pro	Glu	Met	Val	Cys	Gln	Arg	Gln	Tyr	Asp	Ala	Arg	Val	Asp
				185					190					195
Leu	Trp	Ser	Met	Gly	Val	Ile	Leu	Tyr	Glu	Ala	Leu	Phe	Gly	Gln
				200					205					210
Pro	Pro	Phe	Ala	Ser	Arg	Ser	Phe	Ser	Glu	Leu	Glu	Glu	Lys	Ile
				215					220					225
Arg	Ser	Asn	Arg	Val	Ile	Glu	Leu	Pro	Leu	Arg	Pro	Leu	Leu	Ser
				230					235					240
Arg	Asp	Cys	Arg	Asp	Leu	Leu	Gln	Arg	Leu	Leu	Glu	Arg	Asp	Pro
				245					250					255
Ser	Arg	Arg	Ile	Ser	Phe	Gln	Asp	Phe	Phe	Ala	His	Pro	Trp	Val
				260					265					270
Asp	Leu	Glu	His	Met	Pro	Ser	Gly	Glu	Ser	Leu	Gly	Arg	Ala	Thr
				275					280					285
Ala	Leu	Val	Val	Gln	Ala	Val	Lys	Lys	Asp	Gln	Glu	Gly	Asp	Ser
				290					295					300
Ala	Ala	Ala	Leu	Ser	Leu	Tyr	Cys	Lys	Ala	Leu	Asp	Phe	Phe	Val
				305					310					315
Pro	Ala	Leu	His	Tyr	Glu	Val	Asp	Ala	Gln	Arg	Lys	Glu	Ala	Ile
				320					325					330
Lys	Ala	Lys	Val	Gly	Gln	Tyr	Val	Ser	Arg	Ala	Glu	Glu	Leu	Lys
				335					340					345
Ala	Ile	Val	Ser	Ser	Ser	Asn	Gln	Ala	Leu	Leu	Arg	Gln	Gly	Thr
				350					355					360
Ser	Ala	Arg	Asp	Leu	Leu	Arg	Glu	Met	Ala	Arg	Asp	Lys	Pro	Arg
				365					370					375
Leu	Leu	Ala	Ala	Leu	Glu	Val	Ala	Ser	Ala	Ala	Met	Ala	Lys	Glu
				380					385					390
Glu	Ala	Ala	Gly	Gly	Glu	Gln	Asp	Ala	Leu	Asp	Leu	Tyr	Gln	His
				395					400					405
Ser	Leu	Gly	Glu	Leu	Leu	Leu	Leu	Leu	Ala	Ala	Glu	Pro	Pro	Gly
				410					415					420
Arg	Arg	Arg	Glu	Leu	Leu	His	Thr	Glu	Val	Gln	Asn	Leu	Met	Ala
				425					430					435
Arg	Ala	Glu	Tyr	Leu	Lys	Glu	Gln	Met	Arg	Glu	Ser	Arg	Trp	Glu
				440					445					450
Ala	Asp	Thr	Leu	Asp	Lys	Glu	Gly	Leu	Ser	Glu	Ser	Val	Arg	Ser
				455					460					465
Ser	Cys	Thr	Leu	Gln										
				470										

<210> 10

<211> 422

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7477076CD1

<400> 10

Met	Asp	His	Pro	Ser	Arg	Glu	Lys	Asp	Glu	Arg	Gln	Arg	Thr	Thr
1				5					10					15

Lys	Pro	Met	Ala	Gln	Arg	Ser	Ala	His	Cys	Ser	Arg	Pro	Ser	Gly	
				20					25					30	
Ser	Ser	Ser	Ser	Ser	Gly	Val	Leu	Met	Val	Gly	Pro	Asn	Phe	Arg	
				35					40					45	
Val	Gly	Lys	Lys	Ile	Gly	Cys	Gly	Asn	Phe	Gly	Glu	Leu	Arg	Leu	
				50					55					60	
Gly	Lys	Asn	Leu	Tyr	Thr	Asn	Glu	Tyr	Val	Ala	Ile	Lys	Leu	Glu	
				65					70					75	
Pro	Ile	Lys	Ser	Arg	Ala	Pro	Gln	Leu	His	Leu	Glu	Tyr	Arg	Phe	
				80					85					90	
Tyr	Lys	Gln	Leu	Gly	Ser	Ala	Gly	Glu	Gly	Leu	Pro	Gln	Val	Tyr	
				95					100					105	
Tyr	Phe	Gly	Pro	Cys	Gly	Lys	Tyr	Asn	Ala	Met	Val	Leu	Glu	Leu	
				110					115					120	
Leu	Gly	Pro	Ser	Leu	Glu	Asp	Leu	Phe	Asp	Leu	Cys	Asp	Arg	Thr	
				125					130					135	
Phe	Thr	Leu	Lys	Thr	Val	Leu	Met	Ile	Ala	Ile	Gln	Leu	Leu	Ser	
				140					145					150	
Arg	Met	Glu	Tyr	Val	His	Ser	Lys	Asn	Leu	Ile	Tyr	Arg	Asp	Val	
				155					160					165	
Lys	Pro	Glu	Asn	Phe	Leu	Ile	Gly	Arg	Gln	Gly	Asn	Lys	Lys	Glu	
				170					175					180	
His	Val	Ile	His	Ile	Ile	Asp	Phe	Gly	Leu	Ala	Lys	Glu	Tyr	Ile	
				185					190					195	
Asp	Pro	Glu	Thr	Lys	Lys	His	Ile	Pro	Tyr	Arg	Glu	His	Lys	Ser	
				200					205					210	
Leu	Thr	Gly	Thr	Ala	Arg	Tyr	Met	Ser	Ile	Asn	Thr	His	Leu	Gly	
				215					220					225	
Lys	Glu	Gln	Ser	Arg	Arg	Asp	Asp	Leu	Glu	Ala	Leu	Gly	His	Met	
				230					235					240	
Phe	Met	Tyr	Phe	Leu	Arg	Gly	Ser	Leu	Pro	Trp	Gln	Gly	Leu	Lys	
				245					250					255	
Ala	Asp	Thr	Leu	Lys	Glu	Arg	Tyr	Gln	Lys	Ile	Gly	Asp	Thr	Lys	
				260					265					270	
Arg	Asn	Thr	Pro	Ile	Glu	Ala	Leu	Cys	Glu	Asn	Phe	Pro	Glu	Glu	
				275					280					285	
Met	Ala	Thr	Tyr	Leu	Arg	Tyr	Val	Arg	Arg	Leu	Asp	Phe	Phe	Glu	
				290					295					300	
Lys	Pro	Asp	Tyr	Glu	Tyr	Leu	Arg	Thr	Leu	Phe	Thr	Asp	Leu	Phe	
				305					310					315	
Glu	Lys	Lys	Gly	Tyr	Thr	Phe	Asp	Tyr	Ala	Tyr	Asp	Trp	Val	Gly	
				320					325					330	
Arg	Pro	Ile	Pro	Thr	Pro	Val	Gly	Ser	Val	His	Val	Asp	Ser	Gly	
				335					340					345	
Ala	Ser	Ala	Ile	Thr	Arg	Glu	Ser	His	Thr	His	Arg	Asp	Arg	Pro	
				350					355					360	
Ser	Gln	Gln	Gln	Pro	Leu	Arg	Asn	Gln	Val	Val	Ser	Ser	Thr	Asn	
				365					370					375	
Gly	Glu	Leu	Asn	Val	Asp	Asp	Pro	Thr	Gly	Ala	His	Ser	Asn	Ala	
				380					385					390	
Pro	Ile	Thr	Ala	His	Ala	Glu	Val	Glu	Val	Val	Glu	Glu	Ala	Lys	
				395					400					405	
Cys	Cys	Cys	Phe	Phe	Lys	Arg	Lys	Arg	Lys	Lys	Thr	Ala	Gln	Arg	
				410					415					420	

His Lys

<210> 11

<211> 240

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1874092CD1

<400> 11

Met	Pro	Val	Ser	Lys	Cys	Pro	Lys	Lys	Ser	Glu	Ser	Leu	Trp	Lys
1				5					10					15
Gly	Trp	Asp	Arg	Lys	Ala	Gln	Arg	Asn	Gly	Leu	Arg	Ser	Gln	Val
				20					25					30
Tyr	Ala	Val	Asn	Gly	Asp	Tyr	Tyr	Val	Gly	Glu	Trp	Lys	Asp	Asn
				35					40					45
Val	Lys	His	Gly	Lys	Gly	Thr	Gln	Val	Trp	Lys	Lys	Lys	Gly	Ala
				50					55					60
Ile	Tyr	Glu	Gly	Asp	Trp	Lys	Phe	Gly	Lys	Arg	Asp	Gly	Tyr	Gly
				65					70					75
Thr	Leu	Ser	Leu	Pro	Asp	Gln	Gln	Thr	Gly	Lys	Cys	Arg	Arg	Val
				80					85					90
Tyr	Ser	Gly	Trp	Trp	Lys	Gly	Asp	Lys	Lys	Ser	Gly	Tyr	Gly	Ile
				95					100					105
Gln	Phe	Phe	Gly	Pro	Lys	Glu	Tyr	Tyr	Glu	Gly	Asp	Trp	Cys	Gly
				110					115					120
Ser	Gln	Arg	Ser	Gly	Trp	Gly	Arg	Met	Tyr	Tyr	Ser	Asn	Gly	Asp
				125					130					135
Ile	Tyr	Glu	Gly	Gln	Trp	Glu	Asn	Asp	Lys	Pro	Asn	Gly	Glu	Gly
				140					145					150
Met	Leu	Arg	Leu	Lys	Asn	Gly	Asn	Arg	Tyr	Glu	Gly	Cys	Trp	Glu
				155					160					165
Arg	Gly	Met	Lys	Asn	Gly	Ala	Gly	Arg	Phe	Phe	His	Leu	Asp	His
				170					175					180
Gly	Gln	Leu	Phe	Glu	Gly	Phe	Trp	Val	Asp	Asn	Met	Ala	Lys	Cys
				185					190					195
Gly	Thr	Met	Ile	Asp	Phe	Gly	Arg	Asp	Glu	Ala	Pro	Glu	Pro	Thr
				200					205					210
Gln	Phe	Pro	Ile	Pro	Glu	Val	Lys	Ile	Leu	Asp	Pro	Asp	Gly	Val
				215					220					225
Leu	Ala	Glu	Ala	Leu	Ala	Met	Phe	Arg	Lys	Thr	Glu	Glu	Gly	Asp
				230					235					240

<210> 12

<211> 594

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4841542CD1

<400> 12

Met	Lys	Lys	Gln	Ala	Val	Lys	Arg	His	His	His	Lys	His	Asn	Leu
1				5					10					15
Arg	His	Arg	Tyr	Glu	Phe	Leu	Glu	Thr	Leu	Gly	Lys	Gly	Thr	Tyr
				20					25					30
Gly	Lys	Val	Lys	Lys	Ala	Arg	Glu	Ser	Ser	Gly	Arg	Leu	Val	Ala
				35					40					45
Ile	Lys	Ser	Ile	Arg	Lys	Asp	Lys	Ile	Lys	Asp	Glu	Gln	Asp	Leu
				50					55					60
Met	His	Ile	Arg	Arg	Glu	Ile	Glu	Ile	Met	Ser	Ser	Leu	Asn	His
				65					70					75
Pro	His	Ile	Ile	Ala	Ile	His	Glu	Val	Phe	Glu	Asn	Ser	Ser	Lys
				80					85					90
Ile	Val	Ile	Val	Met	Glu	Tyr	Ala	Ser	Arg	Gly	Asp	Leu	Tyr	Asp
				95					100					105
Tyr	Ile	Ser	Glu	Arg	Gln	Gln	Leu	Ser	Glu	Arg	Glu	Ala	Arg	His
				110					115					120
Phe	Phe	Arg	Gln	Ile	Val	Ser	Ala	Val	His	Tyr	Cys	His	Gln	Asn
				125					130					135
Arg	Val	Val	His	Arg	Asp	Leu	Lys	Leu	Glu	Asn	Ile	Leu	Leu	Gly
				140					145					150
Ala	Asn	Gly	Asn	Ile	Lys	Ile	Ala	Asp	Phe	Gly	Leu	Ser	Asn	Leu
				155					160					165
Tyr	His	Gln	Gly	Lys	Phe	Leu	Gln	Thr	Phe	Cys	Gly	Ser	Pro	Leu

Tyr	Ala	Ser	Pro	170	Glu	Ile	Val	Asn	Gly	175	Lys	Pro	Tyr	Thr	Gly	180
				185						190						195
Glu	Val	Asp	Ser	200	Trp	Ser	Leu	Gly	Val	205	Leu	Leu	Tyr	Ile	Leu	210
His	Gly	Thr	Met	215	Pro	Phe	Asp	Gly	His	220	Asp	His	Lys	Ile	Leu	225
Lys	Gln	Ile	Ser	230	Asn	Gly	Ala	Tyr	Arg	235	Glu	Pro	Pro	Lys	Pro	240
Asp	Ala	Cys	Gly	245	Leu	Ile	Arg	Trp	Leu	250	Leu	Met	Val	Asn	Pro	255
Arg	Arg	Ala	Thr	260	Leu	Glu	Asp	Val	Ala	265	Ser	His	Trp	Trp	Val	270
Trp	Gly	Tyr	Ala	275	Thr	Arg	Val	Gly	Glu	280	Gln	Glu	Ala	Pro	His	285
Gly	Gly	His	Pro	290	Gly	Ser	Asp	Ser	Ala	295	Arg	Ala	Ser	Met	Ala	300
Trp	Leu	Arg	Arg	305	Ser	Ser	Arg	Pro	Leu	310	Leu	Glu	Asn	Gly	Ala	315
Val	Cys	Ser	Phe	320	Phe	Lys	Gln	His	Ala	325	Pro	Gly	Gly	Gly	Ser	330
Thr	Pro	Gly	Leu	335	Glu	Arg	Gln	His	Ser	340	Leu	Lys	Lys	Ser	Arg	345
Glu	Asn	Asp	Met	350	Ala	Gln	Ser	Leu	His	355	Ser	Asp	Thr	Ala	Asp	360
Thr	Ala	His	Arg	365	Pro	Gly	Lys	Ser	Asn	370	Leu	Lys	Leu	Pro	Lys	375
Ile	Leu	Lys	Lys	380	Lys	Val	Ser	Ala	Ser	385	Ala	Glu	Gly	Val	Gln	390
Asp	Pro	Pro	Glu	395	Leu	Ser	Pro	Ile	Pro	400	Ala	Ser	Pro	Gly	Gln	405
Ala	Pro	Leu	Leu	410	Pro	Lys	Lys	Gly	Ile	415	Leu	Lys	Lys	Pro	Arg	420
Arg	Glu	Ser	Gly	425	Tyr	Tyr	Ser	Ser	Pro	430	Glu	Pro	Ser	Glu	Ser	435
Glu	Leu	Leu	Asp	440	Ala	Gly	Asp	Val	Phe	445	Val	Ser	Gly	Asp	Pro	450
Glu	Gln	Lys	Pro	455	Pro	Gln	Ala	Ser	Gly	460	Leu	Leu	His	Arg	Gly	465
Gly	Ile	Leu	Lys	470	Leu	Asn	Gly	Lys	Phe	475	Ser	Gln	Thr	Ala	Leu	480
Leu	Ala	Ala	Pro	485	Thr	Thr	Phe	Gly	Ser	490	Leu	Asp	Glu	Leu	Ala	495
Pro	Arg	Pro	Leu	500	Ala	Arg	Ala	Ser	Arg	505	Pro	Ser	Gly	Ala	Val	510
Glu	Asp	Ser	Ile	515	Leu	Ser	Ser	Glu	Ser	520	Phe	Asp	Gln	Leu	Asp	525
Pro	Glu	Arg	Leu	530	Pro	Glu	Pro	Pro	Leu	535	Arg	Gly	Cys	Val	Ser	540
Asp	Asn	Leu	Thr	545	Gly	Leu	Glu	Glu	Pro	550	Pro	Ser	Glu	Gly	Pro	555
Ser	Cys	Leu	Arg	560	Arg	Trp	Arg	Gln	Asp	565	Pro	Leu	Gly	Asp	Ser	570
Phe	Ser	Leu	Thr	575	Asp	Cys	Gln	Glu	Val	580	Thr	Ala	Thr	Tyr	Arg	585
Ala	Leu	Arg	Val	590	Cys	Ser	Lys	Leu	Thr							

<210> 13

<211> 473

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7472695CD1

<400> 13

Met	Ser	Gln	Thr	Ser	Ser	Ile	Gly	Ser	Ala	Glu	Ser	Leu	Ile	Ser
1				5					10					15
Leu	Glu	Arg	Lys	Lys	Glu	Lys	Asn	Ile	Asn	Arg	Asp	Ile	Thr	Ser
				20					25					30
Arg	Lys	Asp	Leu	Pro	Ser	Arg	Thr	Ser	Asn	Val	Glu	Arg	Lys	Ala
				35					40					45
Ser	Gln	Gln	Gln	Trp	Gly	Arg	Gly	Asn	Phe	Thr	Glu	Gly	Lys	Val
				50					55					60
Pro	His	Ile	Arg	Ile	Glu	Asn	Gly	Ala	Ala	Ile	Glu	Glu	Ile	Tyr
				65					70					75
Thr	Phe	Gly	Arg	Ile	Leu	Gly	Lys	Gly	Ser	Phe	Gly	Ile	Val	Ile
				80					85					90
Glu	Ala	Thr	Asp	Lys	Glu	Thr	Glu	Thr	Lys	Trp	Ala	Ile	Lys	Lys
				95					100					105
Val	Asn	Lys	Glu	Lys	Ala	Gly	Ser	Ser	Ala	Val	Lys	Leu	Leu	Glu
				110					115					120
Arg	Glu	Val	Asn	Ile	Leu	Lys	Ser	Val	Lys	His	Glu	His	Ile	Ile
				125					130					135
His	Leu	Glu	Gln	Val	Phe	Glu	Thr	Pro	Lys	Lys	Met	Tyr	Leu	Val
				140					145					150
Met	Glu	Leu	Cys	Glu	Asp	Gly	Glu	Leu	Lys	Glu	Ile	Leu	Asp	Arg
				155					160					165
Lys	Gly	His	Phe	Ser	Glu	Asn	Glu	Thr	Arg	Trp	Ile	Ile	Gln	Ser
				170					175					180
Leu	Ala	Ser	Ala	Ile	Ala	Tyr	Leu	His	Asn	Asn	Asp	Ile	Val	His
				185					190					195
Arg	Asp	Leu	Lys	Leu	Glu	Asn	Ile	Met	Val	Lys	Ser	Ser	Leu	Ile
				200					205					210
Asp	Asp	Asn	Asn	Glu	Ile	Asn	Leu	Asn	Ile	Lys	Val	Thr	Asp	Phe
				215					220					225
Gly	Leu	Ala	Val	Lys	Lys	Gln	Ser	Arg	Ser	Glu	Ala	Met	Leu	Gln
				230					235					240
Ala	Thr	Cys	Gly	Thr	Pro	Ile	Tyr	Met	Ala	Pro	Glu	Val	Ile	Ser
				245					250					255
Ala	His	Asp	Tyr	Ser	Gln	Gln	Cys	Asp	Ile	Trp	Ser	Ile	Gly	Val
				260					265					270
Val	Met	Tyr	Met	Leu	Leu	Arg	Gly	Glu	Pro	Pro	Phe	Leu	Ala	Ser
				275					280					285
Ser	Glu	Glu	Lys	Leu	Phe	Glu	Leu	Ile	Arg	Lys	Gly	Glu	Leu	His
				290					295					300
Phe	Glu	Asn	Ala	Val	Trp	Asn	Ser	Ile	Ser	Asp	Cys	Ala	Lys	Ser
				305					310					315
Val	Leu	Lys	Gln	Leu	Met	Lys	Val	Asp	Pro	Ala	His	Arg	Ile	Thr
				320					325					330
Ala	Lys	Glu	Leu	Leu	Asp	Asn	Gln	Trp	Leu	Thr	Gly	Asn	Lys	Leu
				335					340					345
Ser	Ser	Val	Arg	Pro	Thr	Asn	Val	Leu	Glu	Met	Met	Lys	Glu	Trp
				350					355					360
Lys	Asn	Asn	Pro	Glu	Ser	Val	Glu	Glu	Asn	Thr	Thr	Glu	Glu	Lys
				365					370					375
Asn	Lys	Pro	Ser	Thr	Glu	Glu	Lys	Leu	Lys	Ser	Tyr	Gln	Pro	Trp
				380					385					390
Gly	Asn	Val	Pro	Asp	Ala	Asn	Tyr	Thr	Ser	Asp	Glu	Glu	Glu	Glu
				395					400					405
Lys	Gln	Ser	Thr	Ala	Tyr	Glu	Lys	Gln	Phe	Pro	Ala	Thr	Ser	Lys
				410					415					420
Asp	Asn	Phe	Asp	Met	Cys	Ser	Ser	Ser	Phe	Thr	Ser	Ser	Lys	Leu
				425					430					435
Leu	Pro	Ala	Glu	Ile	Lys	Gly	Glu	Met	Glu	Lys	Thr	Pro	Val	Thr
				440					445					450
Pro	Ser	Gln	Gly	Thr	Ala	Thr	Lys	Tyr	Pro	Ala	Lys	Ser	Gly	Ala
				455					460					465
Leu	Ser	Arg	Thr	Lys	Lys	Lys	Leu							
				470										

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 <213> Homo sapiens

<220>
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<400> 14

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Ala	Ala	Ser	Pro	Ser	Gly	Gly	Arg	Gly	Val	Met	Ala	Ser	Pro	Ala
				20					25					30
Trp	Asp	Arg	Ser	Lys	Gly	Trp	Ser	Gln	Thr	Pro	Gln	Arg	Ala	Asp
				35					40					45
Phe	Val	Ser	Thr	Pro	Leu	Gln	Val	His	Thr	Leu	Arg	Pro	Glu	Asn
				50					55					60
Leu	Leu	Leu	Val	Ser	Thr	Leu	Asp	Gly	Ser	Leu	His	Ala	Leu	Ser
				65					70					75
Lys	Gln	Thr	Gly	Asp	Leu	Lys	Trp	Thr	Leu	Arg	Asp	Asp	Pro	Val
				80					85					90
Ile	Glu	Gly	Pro	Met	Tyr	Val	Thr	Glu	Met	Ala	Phe	Leu	Ser	Asp
				95					100					105
Pro	Ala	Asp	Gly	Ser	Leu	Tyr	Ile	Leu	Gly	Thr	Gln	Lys	Gln	Gln
				110					115					120
Gly	Leu	Met	Lys	Leu	Pro	Phe	Thr	Ile	Pro	Glu	Leu	Val	His	Ala
				125					130					135
Ser	Pro	Cys	Arg	Ser	Ser	Asp	Gly	Val	Phe	Tyr	Thr	Gly	Arg	Lys
				140					145					150
Gln	Asp	Ala	Trp	Phe	Val	Val	Asp	Pro	Glu	Ser	Gly	Glu	Thr	Gln
				155					160					165
Met	Thr	Leu	Thr	Thr	Glu	Gly	Pro	Ser	Thr	Pro	Arg	Leu	Tyr	Ile
				170					175					180
Gly	Arg	Thr	Gln	Tyr	Thr	Val	Thr	Met	His	Asp	Pro	Arg	Ala	Pro
				185					190					195
Ala	Leu	Arg	Trp	Asn	Thr	Thr	Tyr	Arg	Arg	Tyr	Ser	Ala	Pro	Pro
				200					205					210
Met	Asp	Gly	Ser	Pro	Gly	Lys	Tyr	Met	Ser	His	Leu	Ala	Ser	Cys
				215					220					225
Gly	Met	Gly	Leu	Leu	Leu	Thr	Val	Asp	Pro	Gly	Ser	Gly	Thr	Val
				230					235					240
Leu	Trp	Thr	Gln	Asp	Leu	Gly	Val	Pro	Val	Met	Gly	Val	Tyr	Thr
				245					250					255
Trp	His	Gln	Asp	Gly	Leu	Arg	Gln	Leu	Pro	His	Leu	Thr	Leu	Ala
				260					265					270
Arg	Asp	Thr	Leu	His	Phe	Leu	Ala	Leu	Arg	Trp	Gly	His	Ile	Arg
				275					280					285
Leu	Pro	Ala	Ser	Gly	Pro	Arg	Asp	Thr	Ala	Thr	Leu	Phe	Ser	Thr
				290					295					300
Leu	Asp	Thr	Gln	Leu	Leu	Met	Thr	Leu	Tyr	Val	Gly	Lys	Asp	Glu
				305					310					315
Thr	Gly	Phe	Tyr	Val	Ser	Lys	Ala	Leu	Val	His	Thr	Gly	Val	Ala
				320					325					330
Leu	Val	Pro	Arg	Gly	Leu	Thr	Leu	Ala	Pro	Ala	Asp	Gly	Pro	Thr
				335					340					345
Thr	Asp	Glu	Val	Thr	Leu	Gln	Val	Ser	Gly	Glu	Arg	Glu	Gly	Ser
				350					355					360
Pro	Ser	Thr	Ala	Val	Arg	Tyr	Pro	Ser	Gly	Ser	Val	Ala	Leu	Pro
				365					370					375
Ser	Gln	Trp	Leu	Leu	Ile	Gly	His	His	Glu	Leu	Pro	Pro	Val	Leu
				380					385					390
His	Thr	Thr	Met	Leu	Arg	Val	His	Pro	Thr	Leu	Gly	Ser	Gly	Thr
				395					400					405
Ala	Glu	Thr	Arg	Pro	Pro	Glu	Asn	Thr	Gln	Ala	Pro	Ala	Phe	Phe
				410					415					420
Leu	Glu	Leu	Leu	Ser	Leu	Ser	Arg	Glu	Lys	Leu	Trp	Asp	Ser	Glu
				425					430					435

Leu	His	Pro	Glu	Glu	Lys	Thr	Pro	Asp	Ser	Tyr	Leu	Gly	Leu	Gly
				440					445					450
Pro	Gln	Asp	Leu	Leu	Ala	Ala	Ser	Leu	Thr	Ala	Val	Leu	Leu	Gly
				455					460					465
Gly	Trp	Ile	Leu	Phe	Val	Met	Arg	Gln	Gln	Gln	Pro	Gln	Val	Val
				470					475					480
Glu	Lys	Gln	Gln	Glu	Thr	Pro	Leu	Ala	Pro	Ala	Asp	Phe	Ala	His
				485					490					495
Ile	Ser	Gln	Asp	Ala	Gln	Ser	Leu	His	Ser	Gly	Ala	Ser	Arg	Arg
				500					505					510
Ser	Gln	Lys	Arg	Leu	Gln	Ser	Pro	Ser	Lys	Gln	Ala	Gln	Pro	Leu
				515					520					525
Asp	Asp	Pro	Glu	Ala	Glu	Gln	Leu	Thr	Val	Val	Gly	Lys	Ile	Ser
				530					535					540
Phe	Asn	Pro	Lys	Asp	Val	Leu	Gly	Arg	Gly	Ala	Gly	Gly	Thr	Phe
				545					550					555
Val	Phe	Arg	Gly	Gln	Phe	Glu	Gly	Arg	Ala	Val	Ala	Val	Lys	Arg
				560					565					570
Leu	Leu	Arg	Glu	Cys	Phe	Gly	Leu	Val	Arg	Arg	Glu	Val	Gln	Leu
				575					580					585
Leu	Gln	Glu	Ser	Asp	Arg	His	Pro	Asn	Val	Leu	Arg	Tyr	Phe	Cys
				590					595					600
Thr	Glu	Arg	Gly	Pro	Gln	Phe	His	Tyr	Ile	Ala	Leu	Glu	Leu	Cys
				605					610					615
Arg	Ala	Ser	Leu	Gln	Glu	Tyr	Val	Glu	Asn	Pro	Asp	Leu	Asp	Arg
				620					625					630
Gly	Gly	Leu	Glu	Pro	Glu	Val	Val	Leu	Gln	Gln	Leu	Met	Ser	Gly
				635					640					645
Leu	Ala	His	Leu	His	Ser	Leu	His	Ile	Val	His	Arg	Asp	Leu	Lys
				650					655					660
Pro	Gly	Asn	Ile	Leu	Ile	Thr	Gly	Pro	Asp	Ser	Gln	Gly	Leu	Gly
				665					670					675
Arg	Val	Val	Leu	Ser	Asp	Phe	Gly	Leu	Cys	Lys	Lys	Leu	Pro	Ala
				680					685					690
Gly	Arg	Cys	Ser	Phe	Ser	Leu	His	Ser	Gly	Ile	Pro	Gly	Thr	Glu
				695					700					705
Gly	Trp	Met	Ala	Pro	Glu	Leu	Leu	Gln	Leu	Leu	Pro	Pro	Asp	Ser
				710					715					720
Pro	Thr	Ser	Ala	Val	Asp	Ile	Phe	Ser	Ala	Gly	Cys	Val	Phe	Tyr
				725					730					735
Tyr	Val	Leu	Ser	Gly	Gly	Ser	His	Pro	Phe	Gly	Asp	Ser	Leu	Tyr
				740					745					750
Arg	Gln	Ala	Asn	Ile	Leu	Thr	Gly	Ala	Pro	Cys	Leu	Ala	His	Leu
				755					760					765
Glu	Glu	Glu	Val	His	Asp	Lys	Val	Val	Ala	Arg	Asp	Leu	Val	Gly
				770					775					780
Ala	Met	Leu	Ser	Pro	Leu	Pro	Gln	Pro	Arg	Pro	Ser	Ala	Pro	Gln
				785					790					795
Val	Leu	Ala	His	Pro	Phe	Phe	Trp	Ser	Arg	Ala	Lys	Gln	Leu	Gln
				800					805					810
Phe	Phe	Gln	Asp	Val	Ser	Asp	Trp	Leu	Glu	Lys	Glu	Ser	Glu	Gln
				815					820					825
Glu	Pro	Leu	Val	Arg	Ala	Leu	Glu	Ala	Gly	Gly	Cys	Ala	Val	Val
				830					835					840
Arg	Asp	Asn	Trp	His	Glu	His	Ile	Ser	Met	Pro	Leu	Gln	Thr	Asp
				845					850					855
Leu	Arg	Lys	Phe	Arg	Ser	Tyr	Lys	Gly	Thr	Ser	Val	Arg	Asp	Leu
				860					865					870
Leu	Arg	Ala	Val	Arg	Asn	Lys	Lys	His	His	Tyr	Arg	Glu	Leu	Pro
				875					880					885
Val	Glu	Val	Arg	Gln	Ala	Leu	Gly	Gln	Val	Pro	Asp	Gly	Phe	Val
				890					895					900
Gln	Tyr	Phe	Thr	Asn	Arg	Phe	Pro	Arg	Leu	Leu	Leu	His	Thr	His
				905					910					915
Arg	Ala	Met	Arg	Ser	Cys	Ala	Ser	Glu	Ser	Leu	Phe	Leu	Pro	Tyr
				920					925					930
Tyr	Pro	Pro	Asp	Ser	Glu	Ala	Arg	Arg	Pro	Cys	Pro	Gly	Ala	Thr

Gly Arg 935 940 945
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 <223> Incyte ID No: 7163416CD1
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 Gln Asn Phe Gln His Arg Val His Thr Ser Phe Asp Pro Lys Glu
 20 25 30
 Gly Lys Phe Val Gly Leu Pro Pro Gln Trp Gln Asn Ile Leu Asp
 35 40 45
 Thr Leu Arg Arg Pro Lys Pro Val Val Asp Pro Ser Arg Ile Thr
 50 55 60
 Arg Val Gln Leu Gln Pro Met Lys Thr Val Val Arg Gly Ser Ala
 65 70 75
 Met Pro Val Asp Gly Tyr Ile Ser Gly Leu Leu Asn Asp Ile Gln
 80 85 90
 Lys Leu Ser Val Ile Ser Ser Asn Thr Leu Arg Gly Arg Ser Pro
 95 100 105
 Thr Ser Arg Arg Arg Ala Gln Ser Leu Gly Leu Leu Gly Asp Glu
 110 115 120
 His Trp Ala Thr Asp Pro Asp Met Tyr Leu Gln Ser Pro Gln Ser
 125 130 135
 Glu Arg Thr Asp Pro His Gly Leu Tyr Leu Ser Cys Asn Gly Gly
 140 145 150
 Thr Pro Ala Gly His Lys Gln Met Pro Trp Pro Glu Pro Gln Ser
 155 160 165
 Pro Arg Val Leu Pro Asn Gly Leu Ala Ala Lys Ala Gln Ser Leu
 170 175 180
 Gly Pro Ala Glu Phe Gln Gly Ala Ser Gln Arg Cys Leu Gln Leu
 185 190 195
 Gly Ala Cys Leu Gln Ser Ser Pro Pro Gly Ala Ser Pro Pro Thr
 200 205 210
 Gly Thr Asn Arg His Gly Met Lys Ala Ala Lys His Gly Ser Glu
 215 220 225
 Glu Ala Arg Pro Gln Ser Cys Leu Val Gly Ser Ala Thr Gly Arg
 230 235 240
 Pro Gly Gly Glu Gly Ser Pro Ser Pro Lys Thr Arg Glu Ser Ser
 245 250 255
 Leu Lys Arg Arg Leu Phe Arg Ser Met Phe Leu Ser Thr Ala Ala
 260 265 270
 Thr Ala Pro Pro Ser Ser Ser Lys Pro Gly Pro Pro Pro Gln Ser
 275 280 285
 Lys Pro Asn Ser Ser Phe Arg Pro Pro Gln Lys Asp Asn Pro Pro
 290 295 300
 Ser Leu Val Ala Lys Ala Gln Ser Leu Pro Ser Asp Gln Pro Val
 305 310 315
 Gly Thr Phe Ser Pro Leu Thr Thr Ser Asp Thr Ser Ser Pro Gln
 320 325 330
 Lys Ser Leu Arg Thr Ala Pro Ala Thr Gly Gln Leu Pro Gly Arg
 335 340 345
 Ser Ser Pro Ala Gly Ser Pro Arg Thr Trp His Ala Gln Ile Ser
 350 355 360
 Thr Ser Asn Leu Tyr Leu Pro Gln Asp Pro Thr Val Ala Lys Gly
 365 370 375
 Ala Leu Ala Gly Glu Asp Thr Gly Val Val Thr His Glu Gln Phe
 380 385 390
 Lys Ala Ala Leu Arg Met Val Val Asp Gln Gly Asp Pro Arg Leu

Leu	Leu	Asp	Ser	395	Tyr	Val	Lys	Ile	Gly	400	Glu	Gly	Ser	Thr	Gly	405	Ile
Val	Cys	Leu	Ala	410	Arg	Glu	Lys	His	Ser	415	Gly	Arg	Gln	Val	Ala	420	Val
Lys	Met	Met	Asp	425	Leu	Arg	Lys	Gln	Gln	430	Arg	Arg	Glu	Leu	Leu	435	Phe
Asn	Glu	Val	Val	440	Ile	Met	Arg	Asp	Tyr	445	Gln	His	Phe	Asn	Val	450	Val
Glu	Met	Tyr	Lys	455	Ser	Tyr	Leu	Val	Gly	460	Glu	Glu	Leu	Trp	Val	465	Leu
Met	Glu	Phe	Leu	470	Gln	Gly	Gly	Ala	Leu	475	Thr	Asp	Ile	Val	Ser	480	Gln
Val	Arg	Leu	Asn	485	Glu	Glu	Gln	Ile	Ala	490	Thr	Val	Cys	Glu	Ala	495	Val
Leu	Gln	Ala	Leu	500	Ala	Tyr	Leu	His	Ala	505	Gln	Gly	Val	Ile	His	510	Arg
Asp	Ile	Lys	Ser	515	Asp	Ser	Ile	Leu	Leu	520	Thr	Leu	Asp	Gly	Arg	525	Val
Lys	Leu	Ser	Asp	530	Phe	Gly	Phe	Cys	Ala	535	Gln	Ile	Ser	Lys	Asp	540	Val
Pro	Lys	Arg	Lys	545	Ser	Leu	Val	Gly	Thr	550	Pro	Tyr	Trp	Met	Ala	555	Pro
Glu	Val	Ile	Ser	560	Arg	Ser	Leu	Tyr	Ala	565	Thr	Glu	Val	Asp	Ile	570	Trp
Ser	Leu	Gly	Ile	575	Met	Val	Ile	Glu	Met	580	Val	Asp	Gly	Glu	Pro	585	Pro
Tyr	Phe	Ser	Asp	590	Ser	Pro	Val	Gln	Ala	595	Met	Lys	Arg	Leu	Arg	600	Asp
Ser	Pro	Pro	Pro	605	Lys	Leu	Lys	Asn	Ser	610	His	Lys	Val	Ser	Trp	615	His
Thr	Arg	Val	Arg	620	Arg	Arg	Pro	His	Ser	625	Ser	Ser				630	
				635						640							

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<211> 576

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7472822CD1

<400> 16

Met	Pro	Ala	Leu	Ser	Thr	Gly	Ser	Gly	Ser	Asp	Thr	Gly	Leu	Tyr
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Glu	Leu	Leu	Ala	Ala	Leu	Pro	Ala	Gln	Leu	Gln	Pro	His	Val	Asp
				20					25					30
Ser	Gln	Glu	Asp	Leu	Thr	Phe	Leu	Trp	Asp	Met	Phe	Gly	Glu	Lys
				35					40					45
Ser	Leu	His	Ser	Leu	Val	Lys	Ile	His	Glu	Lys	Leu	His	Tyr	Tyr
				50					55					60
Glu	Lys	Gln	Ser	Pro	Val	Pro	Ile	Leu	His	Gly	Ala	Ala	Ala	Leu
				65					70					75
Ala	Asp	Asp	Leu	Ala	Glu	Glu	Leu	Gln	Asn	Lys	Pro	Leu	Asn	Ser
				80					85					90
Glu	Ile	Arg	Glu	Leu	Leu	Lys	Leu	Leu	Ser	Lys	Pro	Asn	Val	Lys
				95					100					105
Ala	Leu	Leu	Ser	Val	His	Asp	Thr	Val	Ala	Gln	Lys	Asn	Tyr	Asp
				110					115					120
Pro	Val	Leu	Pro	Pro	Met	Pro	Glu	Asp	Ile	Asp	Asp	Glu	Glu	Asp
				125					130					135
Ser	Val	Lys	Ile	Ile	Arg	Leu	Val	Lys	Asn	Arg	Glu	Pro	Leu	Gly
				140					145					150
Ala	Thr	Ile	Lys	Lys	Asp	Glu	Gln	Thr	Gly	Ala	Ile	Ile	Val	Ala
				155					160					165
Arg	Ile	Met	Arg	Gly	Gly	Ala	Ala	Asp	Arg	Ser	Gly	Leu	Ile	His

Val Gly Asp Glu	170	Arg Glu Val Asn	175	Gly Ile Pro Val Glu	180
Lys Arg Pro Glu	185	Glu Ile Ile Gln Ile	190	Leu Ala Gln Ser Gln	195
Ala Ile Thr Phe	200	Lys Ile Ile Pro Gly	205	Ser Lys Glu Glu Thr	210
Ser Lys Glu Gly	215	Lys Met Phe Ile Lys	220	Ala Leu Phe Asp Tyr	225
Pro Asn Glu Asp	230	Lys Ala Ile Pro Cys	235	Lys Glu Ala Gly Leu	240
Phe Lys Lys Gly	245	Asp Ile Leu Gln Ile	250	Met Ser Gln Asp Asp	255
Thr Trp Trp Gln	260	Ala Lys His Glu Ala	265	Asp Ala Asn Pro Arg	270
Gly Leu Ile Pro	275	Ser Lys His Phe Gln	280	Glu Arg Arg Leu Ala	285
Arg Arg Pro Glu	290	Ile Leu Val Gln Pro	295	Lys Val Ser Asn Arg	300
Lys Ser Ser Gly	305	Phe Arg Lys Ser Phe	310	Arg Leu Ser Arg Lys	315
Lys Lys Thr Asn	320	Lys Ser Met Tyr Glu	325	Cys Lys Lys Ser Asp	330
Tyr Asp Thr Ala	335	Asp Val Pro Thr Tyr	340	Glu Glu Val Thr Pro	345
Arg Arg Gln Thr	350	Asn Glu Lys Tyr Arg	355	Leu Val Val Leu Val	360
Pro Val Gly Val	365	Glu Asn Glu Leu Lys	370	Arg Lys Leu Leu Ile	375
Ser Asp Thr Gln	380	His Tyr Gly Val Thr	385	Val Pro His Thr Thr	390
Ala Arg Arg Ser	395	Glu Ser Asp Gly Val	400	Glu Tyr Ile Phe Ile	405
Ser Lys His Leu	410	Phe Glu Thr Asp Val	415	Gln Asn Asn Lys Phe	420
Glu Tyr Gly Glu	425	Tyr Lys Asn Asn Tyr	430	Tyr Gly Thr Ser Ile	435
Ser Val Arg Ser	440	Val Leu Ala Lys Asn	445	Lys Val Cys Leu Leu	450
Val Gln Pro His	455	Thr Val Lys His Leu	460	Arg Thr Leu Glu Phe	465
Pro Tyr Val Ile	470	Phe Ile Lys Pro Pro	475	Ser Ile Glu Arg Leu	480
Glu Thr Arg Lys	485	Asn Ala Lys Ile Ile	490	Ser Ser Arg Asp Asp	495
Gly Ala Ala Lys	500	Pro Phe Thr Glu Glu	505	Asp Phe Gln Glu Met	510
Lys Ser Ala Gln	515	Ile Met Glu Ser Gln	520	Tyr Gly His Leu Phe	525
Lys Ile Ile Ile	530	Asn Asp Asp Leu Thr	535	Val Ala Phe Asn Glu	540
Lys Thr Thr Phe	545	Asp Lys Leu Glu Thr	550	Glu Thr His Trp Val	555
Val Ser Trp Leu	560	His Ser	565		570
	575				

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<400> 17
 Met Val Ala Gly Leu Thr Leu Gly Lys Gly Pro Glu Ser Pro Asp

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Gly Asp Val Ser Val	Pro Glu Arg Lys Asp	Glu Val Ala Gly Gly	
20	25	30	
Gly Gly Glu Glu Glu	Glu Ala Glu Glu Arg	Gly Arg His Ala Gln	
35	40	45	
Tyr Val Gly Pro Tyr	Arg Leu Glu Lys Thr	Leu Gly Lys Gly Gln	
50	55	60	
Thr Gly Leu Val Lys	Leu Gly Val His Cys	Ile Thr Gly Gln Lys	
65	70	75	
Val Ala Ile Lys Ile	Val Asn Arg Glu Lys	Leu Ser Glu Ser Val	
80	85	90	
Leu Met Lys Val Glu	Arg Glu Ile Ala Ile	Leu Lys Leu Ile Glu	
95	100	105	
His Pro His Val Leu	Lys Leu His Asp Val	Tyr Glu Asn Lys Lys	
110	115	120	
Tyr Leu Tyr Leu Val	Leu Glu His Val Ser	Gly Gly Glu Leu Phe	
125	130	135	
Asp Tyr Leu Val Lys	Lys Gly Arg Leu Thr	Pro Lys Glu Ala Arg	
140	145	150	
Lys Phe Phe Arg Gln	Ile Val Ser Ala Leu	Asp Phe Cys His Ser	
155	160	165	
Tyr Ser Ile Cys His	Arg Asp Leu Lys Pro	Glu Asn Leu Leu Leu	
170	175	180	
Asp Glu Lys Asn Asn	Ile Arg Ile Ala Asp	Phe Gly Met Ala Ser	
185	190	195	
Leu Gln Val Gly Asp	Ser Leu Leu Glu Thr	Ser Cys Gly Ser Pro	
200	205	210	
His Tyr Ala Cys Pro	Glu Val Ile Lys Gly	Glu Lys Tyr Asp Gly	
215	220	225	
Arg Arg Ala Asp Met	Trp Ser Cys Gly Val	Ile Leu Phe Ala Leu	
230	235	240	
Leu Val Gly Ala Leu	Pro Phe Asp Asp Asp	Asn Leu Arg Gln Leu	
245	250	255	
Leu Glu Lys Val Lys	Arg Gly Val Phe His	Met Pro His Phe Ile	
260	265	270	
Pro Pro Asp Cys Gln	Ser Leu Leu Arg Gly	Met Ile Glu Val Glu	
275	280	285	
Pro Glu Lys Arg Leu	Ser Leu Glu Gln Ile	Gln Lys His Pro Trp	
290	295	300	
Tyr Leu Gly Gly Lys	His Glu Pro Asp Pro	Cys Leu Glu Pro Ala	
305	310	315	
Pro Gly Arg Arg Val	Ala Met Arg Ser Leu	Pro Ser Asn Gly Glu	
320	325	330	
Leu Asp Pro Asp Val	Leu Glu Ser Met Ala	Ser Leu Gly Cys Phe	
335	340	345	
Arg Asp Arg Glu Arg	Leu His Arg Glu Leu	Arg Ser Glu Glu Glu	
350	355	360	
Asn Gln Glu Lys Met	Ile Tyr Tyr Leu Leu	Leu Asp Arg Lys Glu	
365	370	375	
Arg Tyr Pro Ser Cys	Glu Asp Gln Asp Leu	Pro Pro Arg Asn Asp	
380	385	390	
Val Asp Pro Pro Arg	Lys Arg Val Asp Ser	Pro Met Leu Ser Arg	
395	400	405	
His Gly Lys Arg Arg	Pro Glu Arg Lys Ser	Met Glu Val Leu Ser	
410	415	420	
Ile Thr Asp Ala Gly	Gly Gly Gly Ser Pro	Val Pro Thr Arg Arg	
425	430	435	
Ala Leu Glu Met Ala	Gln His Ser Gln Arg	Ser Arg Ser Val Ser	
440	445	450	
Gly Ala Ser Thr Gly	Leu Ser Ser Ser Pro	Leu Ser Ser Pro Arg	
455	460	465	
Ser Pro Val Phe Ser	Phe Ser Pro Glu Pro	Gly Ala Gly Asp Glu	
470	475	480	
Ala Arg Gly Gly Gly	Ser Pro Thr Ser Lys	Thr Gln Thr Leu Pro	
485	490	495	
Ser Arg Gly Pro Arg	Gly Gly Gly Ala Gly	Glu Gln Pro Pro Pro	
500	505	510	

Pro	Ser	Ala	Arg	Ser	Thr	Pro	Leu	Pro	Gly	Pro	Pro	Gly	Ser	Pro
				515					520					525
Arg	Ser	Ser	Gly	Gly	Thr	Pro	Leu	His	Ser	Pro	Leu	His	Thr	Pro
				530					535					540
Arg	Ala	Ser	Pro	Thr	Gly	Thr	Pro	Gly	Thr	Thr	Pro	Pro	Pro	Ser
				545					550					555
Pro	Gly	Gly	Gly	Val	Gly	Gly	Ala	Ala	Trp	Arg	Ser	Arg	Leu	Asn
				560					565					570
Ser	Ile	Arg	Asn	Ser	Phe	Leu	Gly	Ser	Pro	Arg	Phe	His	Arg	Arg
				575					580					585
Lys	Met	Gln	Val	Pro	Thr	Ala	Glu	Glu	Met	Ser	Ser	Leu	Thr	Pro
				590					595					600
Glu	Ser	Ser	Pro	Glu	Leu	Ala	Lys	Arg	Ser	Trp	Phe	Gly	Asn	Phe
				605					610					615
Ile	Ser	Leu	Asp	Lys	Glu	Glu	Gln	Ile	Phe	Leu	Val	Leu	Lys	Asp
				620					625					630
Lys	Pro	Leu	Ser	Ser	Ile	Lys	Ala	Asp	Ile	Val	His	Ala	Phe	Leu
				635					640					645
Ser	Ile	Pro	Ser	Leu	Ser	His	Ser	Val	Leu	Ser	Gln	Thr	Ser	Phe
				650					655					660
Arg	Ala	Glu	Tyr	Lys	Ala	Ser	Gly	Gly	Pro	Ser	Val	Phe	Gln	Lys
				665					670					675
Pro	Val	Arg	Phe	Gln	Val	Asp	Ile	Ser	Ser	Ser	Glu	Gly	Pro	Glu
				680					685					690
Pro	Ser	Pro	Arg	Arg	Asp	Gly	Ser	Gly	Gly	Gly	Gly	Ile	Tyr	Ser
				695					700					705
Val	Thr	Phe	Thr	Leu	Ile	Ser	Gly	Pro	Ser	Arg	Arg	Phe	Lys	Arg
				710					715					720
Val	Val	Glu	Thr	Ile	Gln	Ala	Gln	Leu	Leu	Ser	Thr	His	Asp	Gln
				725					730					735
Pro	Ser	Val	Gln	Ala	Leu	Ala	Asp	Glu	Lys	Asn	Gly	Ala	Gln	Thr
				740					745					750
Arg	Pro	Ala	Gly	Ala	Pro	Pro	Arg	Ser	Leu	Gln	Pro	Pro	Pro	Gly
				755					760					765
Arg	Pro	Asp	Pro	Glu	Leu	Ser	Ser	Ser	Pro	Arg	Arg	Gly	Pro	Pro
				770					775					780
Lys	Asp	Lys	Lys	Leu	Leu	Ala	Thr	Asn	Gly	Thr	Pro	Leu	Pro	
				785					790					

<210> 18

<211> 504

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3773709CD1

<400> 18

Met	Ser	Gly	Leu	Leu	Thr	Asp	Pro	Glu	Gln	Arg	Ala	Gln	Glu	Pro
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Arg	Tyr	Pro	Gly	Phe	Val	Leu	Gly	Leu	Asp	Val	Gly	Ser	Ser	Val
				20					25					30
Ile	Arg	Cys	His	Val	Tyr	Asp	Arg	Ala	Ala	Arg	Val	Cys	Gly	Ser
				35					40					45
Ser	Val	Gln	Lys	Val	Glu	Asn	Leu	Tyr	Pro	Gln	Ile	Gly	Trp	Val
				50					55					60
Glu	Ile	Asp	Pro	Asp	Val	Leu	Trp	Ile	Gln	Phe	Val	Ala	Val	Ile
				65					70					75
Lys	Glu	Ala	Val	Lys	Ala	Ala	Gly	Ile	Gln	Met	Asn	Gln	Ile	Val
				80					85					90
Gly	Leu	Gly	Ile	Ser	Thr	Gln	Arg	Ala	Thr	Phe	Ile	Thr	Trp	Asn
				95					100					105
Lys	Lys	Thr	Gly	Asn	His	Phe	His	Asn	Phe	Ile	Ser	Trp	Gln	Asp
				110					115					120
Leu	Arg	Ala	Val	Glu	Leu	Val	Lys	Ser	Trp	Asn	Asn	Ser	Leu	Leu
				125					130					135

Met	Lys	Ile	Phe	His	Ser	Ser	Cys	Arg	Val	Leu	His	Phe	Phe	Thr
				140					145					150
Arg	Ser	Lys	Arg	Leu	Phe	Thr	Ala	Ser	Leu	Phe	Thr	Phe	Thr	Thr
				155					160					165
Gln	Gln	Thr	Ser	Leu	Arg	Leu	Val	Trp	Ile	Leu	Gln	Asn	Leu	Thr
				170					175					180
Glu	Val	Gln	Lys	Ala	Val	Glu	Glu	Glu	Asn	Cys	Cys	Phe	Gly	Thr
				185					190					195
Ile	Asp	Thr	Trp	Trp	Leu	Tyr	Lys	Leu	Thr	Lys	Gly	Ser	Val	Tyr
				200					205					210
Ala	Thr	Asp	Phe	Ser	Asn	Ala	Ser	Thr	Thr	Gly	Leu	Phe	Asp	Pro
				215					220					225
Tyr	Ser	His	Asn	Phe	Gly	Ser	Val	Asp	Glu	Ile	Phe	Gly	Val	
				230					235					240
Pro	Ile	Pro	Ile	Val	Ala	Leu	Val	Ala	Asp	Gln	Gln	Ser	Ala	Met
				245					250					255
Phe	Gly	Glu	Cys	Cys	Phe	Gln	Thr	Gly	Asp	Val	Lys	Leu	Thr	Met
				260					265					270
Gly	Thr	Gly	Thr	Phe	Leu	Asp	Ile	Asn	Thr	Gly	Asn	Ser	Leu	Gln
				275					280					285
Gln	Thr	Thr	Gly	Gly	Phe	Tyr	Pro	Leu	Ile	Gly	Trp	Lys	Ile	Gly
				290					295					300
Gln	Glu	Val	Val	Cys	Leu	Ala	Glu	Ser	Asn	Ala	Gly	Asp	Thr	Gly
				305					310					315
Thr	Ala	Ile	Lys	Trp	Ala	Gln	Gln	Leu	Asp	Leu	Phe	Thr	Asp	Ala
				320					325					330
Ala	Glu	Thr	Glu	Lys	Met	Ala	Lys	Ser	Leu	Glu	Asp	Ser	Glu	Gly
				335					340					345
Val	Cys	Phe	Val	Pro	Ser	Phe	Ser	Gly	Leu	Gln	Ala	Pro	Leu	Asn
				350					355					360
Asp	Pro	Trp	Ala	Cys	Ala	Ser	Phe	Met	Gly	Leu	Lys	Pro	Ser	Thr
				365					370					375
Ser	Lys	Tyr	His	Leu	Val	Arg	Ala	Ile	Leu	Glu	Ser	Ile	Ala	Phe
				380					385					390
Arg	Asn	Lys	Gln	Leu	Tyr	Glu	Met	Met	Lys	Lys	Glu	Ile	His	Ile
				395					400					405
Pro	Val	Arg	Lys	Ile	Arg	Ala	Asp	Gly	Gly	Val	Cys	Lys	Asn	Gly
				410					415					420
Phe	Val	Met	Gln	Met	Thr	Ser	Asp	Leu	Ile	Asn	Glu	Asn	Ile	Asp
				425					430					435
Arg	Pro	Ala	Asp	Ile	Asp	Met	Ser	Cys	Leu	Gly	Ala	Ala	Ser	Leu
				440					445					450
Ala	Gly	Leu	Ala	Val	Gly	Phe	Trp	Thr	Asp	Lys	Glu	Glu	Leu	Lys
				455					460					465
Lys	Leu	Arg	Gln	Ser	Glu	Val	Val	Phe	Lys	Pro	Gln	Lys	Lys	Cys
				470					475					480
Gln	Glu	Tyr	Glu	Met	Ser	Leu	Glu	Asn	Trp	Ala	Lys	Ala	Val	Lys
				485					490					495
Arg	Ser	Met	Asn	Trp	Tyr	Asn	Lys	Thr						
				500										

<210> 19

<211> 553

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7477204CD1

<400> 19

Met	Val	Asp	Met	Gly	Ala	Leu	Asp	Asn	Leu	Ile	Ala	Asn	Thr	Ala
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Tyr	Leu	Gln	Ala	Arg	Lys	Pro	Ser	Asp	Cys	Asp	Ser	Lys	Glu	Leu
				20					25					30
Gln	Arg	Arg	Arg	Arg	Ser	Leu	Ala	Leu	Pro	Gly	Leu	Gln	Gly	Cys
				35					40					45

Ala	Glu	Leu	Arg	Gln	Lys	Leu	Ser	Leu	Asn	Phe	His	Ser	Leu	Cys
				50					55					60
Glu	Gln	Gln	Pro	Ile	Gly	Arg	Arg	Leu	Phe	Arg	Asp	Phe	Leu	Ala
				65					70					75
Thr	Val	Pro	Thr	Phe	Arg	Lys	Ala	Ala	Thr	Phe	Leu	Glu	Asp	Val
				80					85					90
Gln	Asn	Trp	Glu	Leu	Ala	Glu	Glu	Gly	Pro	Thr	Lys	Asp	Ser	Ala
				95					100					105
Leu	Gln	Gly	Leu	Val	Ala	Thr	Cys	Ala	Ser	Ala	Pro	Ala	Pro	Gly
				110					115					120
Asn	Pro	Gln	Pro	Phe	Leu	Ser	Gln	Ala	Val	Ala	Thr	Lys	Cys	Gln
				125					130					135
Ala	Ala	Thr	Thr	Glu	Glu	Glu	Arg	Val	Ala	Ala	Val	Thr	Leu	Ala
				140					145					150
Lys	Ala	Glu	Ala	Met	Ala	Phe	Leu	Gln	Glu	Gln	Pro	Phe	Lys	Asp
				155					160					165
Phe	Val	Thr	Ser	Ala	Phe	Tyr	Asp	Lys	Phe	Leu	Gln	Trp	Lys	Leu
				170					175					180
Phe	Glu	Met	Gln	Pro	Val	Ser	Asp	Lys	Tyr	Phe	Thr	Glu	Phe	Arg
				185					190					195
Val	Leu	Gly	Lys	Gly	Gly	Phe	Gly	Glu	Val	Cys	Ala	Val	Gln	Val
				200					205					210
Lys	Asn	Thr	Gly	Lys	Met	Tyr	Ala	Cys	Lys	Lys	Leu	Asp	Lys	Lys
				215					220					225
Arg	Leu	Lys	Lys	Lys	Gly	Gly	Glu	Lys	Met	Ala	Leu	Leu	Glu	Lys
				230					235					240
Glu	Ile	Leu	Glu	Lys	Val	Ser	Ser	Pro	Phe	Ile	Val	Ser	Leu	Ala
				245					250					255
Tyr	Ala	Phe	Glu	Ser	Lys	Thr	His	Leu	Cys	Leu	Val	Met	Ser	Leu
				260					265					270
Met	Asn	Gly	Gly	Asp	Leu	Lys	Phe	His	Ile	Tyr	Asn	Val	Gly	Thr
				275					280					285
Arg	Gly	Leu	Asp	Met	Ser	Arg	Val	Ile	Phe	Tyr	Ser	Ala	Gln	Ile
				290					295					300
Ala	Cys	Gly	Met	Leu	His	Leu	His	Glu	Leu	Gly	Ile	Val	Tyr	Arg
				305					310					315
Asp	Met	Lys	Pro	Glu	Asn	Val	Leu	Leu	Asp	Asp	Leu	Gly	Asn	Cys
				320					325					330
Arg	Leu	Ser	Asp	Leu	Gly	Leu	Ala	Val	Glu	Met	Lys	Gly	Gly	Lys
				335					340					345
Pro	Ile	Thr	Gln	Arg	Ala	Gly	Thr	Asn	Gly	Tyr	Met	Ala	Pro	Glu
				350					355					360
Ile	Leu	Met	Glu	Lys	Val	Ser	Tyr	Ser	Tyr	Pro	Val	Asp	Trp	Phe
				365					370					375
Ala	Met	Gly	Cys	Ser	Ile	Tyr	Glu	Met	Val	Ala	Gly	Arg	Thr	Pro
				380					385					390
Phe	Lys	Asp	Tyr	Lys	Glu	Lys	Val	Ser	Lys	Glu	Asp	Leu	Lys	Gln
				395					400					405
Arg	Thr	Leu	Gln	Asp	Glu	Val	Lys	Phe	Gln	His	Asp	Asn	Phe	Thr
				410					415					420
Glu	Glu	Ala	Lys	Asp	Ile	Cys	Arg	Leu	Phe	Leu	Ala	Lys	Lys	Pro
				425					430					435
Glu	Gln	Arg	Leu	Gly	Ser	Arg	Glu	Lys	Ser	Asp	Asp	Pro	Arg	Lys
				440					445					450
His	His	Phe	Phe	Lys	Thr	Ile	Asn	Phe	Pro	Arg	Leu	Glu	Ala	Gly
				455					460					465
Leu	Ile	Glu	Pro	Pro	Phe	Val	Pro	Asp	Pro	Ser	Val	Val	Tyr	Ala
				470					475					480
Lys	Asp	Ile	Ala	Glu	Ile	Asp	Asp	Phe	Ser	Glu	Val	Arg	Gly	Val
				485					490					495
Glu	Phe	Asp	Asp	Lys	Asp	Lys	Gln	Phe	Phe	Lys	Asn	Phe	Ala	Thr
				500					505					510
Gly	Ala	Val	Pro	Ile	Ala	Trp	Gln	Glu	Glu	Ile	Ile	Glu	Thr	Gly
				515					520					525
Leu	Phe	Glu	Glu	Leu	Asn	Asp	Pro	Asn	Arg	Pro	Thr	Gly	Cys	Glu
				530					535					540
Glu	Gly	Asn	Ser	Ser	Lys	Ser	Gly	Val	Cys	Leu	Leu	Leu		

545

550

<210> 20
 <211> 871
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 3016969CD1

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Pro	Cys	Ser	Ser	Pro	Gly	Ser	Ala	Ser	Gln	Ala	Ser	Ser	Ser	Gln
				20					25					30
Val	Ser	Ser	Leu	Arg	Val	Gly	Ser	Ser	Gln	Val	Gly	Thr	Glu	Pro
				35					40					45
Gly	Pro	Ser	Leu	Asp	Ala	Glu	Gly	Trp	Thr	Gln	Glu	Ala	Glu	Asp
				50					55					60
Leu	Ser	Asp	Ser	Thr	Pro	Thr	Leu	Gln	Arg	Pro	Gln	Glu	Gln	Val
				65					70					75
Thr	Met	Arg	Lys	Phe	Ser	Leu	Gly	Gly	Arg	Gly	Gly	Tyr	Ala	Gly
				80					85					90
Val	Ala	Gly	Tyr	Gly	Thr	Phe	Ala	Phe	Gly	Gly	Asp	Ala	Gly	Gly
				95					100					105
Met	Leu	Gly	Gln	Gly	Pro	Met	Trp	Ala	Arg	Ile	Ala	Trp	Ala	Val
				110					115					120
Ser	Gln	Ser	Glu	Glu	Glu	Glu	Gln	Glu	Glu	Ala	Arg	Ala	Glu	Ser
				125					130					135
Gln	Ser	Glu	Glu	Gln	Gln	Glu	Ala	Arg	Ala	Glu	Ser	Pro	Leu	Pro
				140					145					150
Gln	Val	Ser	Ala	Arg	Pro	Val	Pro	Glu	Val	Gly	Arg	Ala	Pro	Thr
				155					160					165
Arg	Ser	Ser	Pro	Glu	Pro	Thr	Pro	Trp	Glu	Asp	Ile	Gly	Gln	Val
				170					175					180
Ser	Leu	Val	Gln	Ile	Arg	Asp	Leu	Ser	Gly	Asp	Ala	Glu	Ala	Ala
				185					190					195
Asp	Thr	Ile	Ser	Leu	Asp	Ile	Ser	Glu	Val	Asp	Pro	Ala	Tyr	Leu
				200					205					210
Asn	Leu	Ser	Asp	Leu	Tyr	Asp	Ile	Lys	Tyr	Leu	Pro	Phe	Glu	Phe
				215					220					225
Met	Ile	Phe	Arg	Lys	Val	Pro	Lys	Ser	Ala	Gln	Pro	Glu	Pro	Pro
				230					235					240
Ser	Pro	Met	Ala	Glu	Glu	Glu	Leu	Ala	Glu	Phe	Pro	Glu	Pro	Thr
				245					250					255
Trp	Pro	Trp	Pro	Gly	Glu	Leu	Gly	Pro	His	Ala	Gly	Leu	Glu	Ile
				260					265					270
Thr	Glu	Glu	Ser	Glu	Asp	Val	Asp	Ala	Leu	Leu	Ala	Glu	Ala	Ala
				275					280					285
Val	Gly	Arg	Lys	Arg	Lys	Trp	Ser	Ser	Pro	Ser	Arg	Ser	Leu	Phe
				290					295					300
His	Phe	Pro	Gly	Arg	His	Leu	Pro	Leu	Asp	Glu	Pro	Ala	Glu	Leu
				305					310					315
Gly	Leu	Arg	Glu	Arg	Val	Lys	Ala	Ser	Val	Glu	His	Ile	Ser	Arg
				320					325					330
Ile	Leu	Lys	Gly	Arg	Pro	Glu	Gly	Leu	Glu	Lys	Glu	Gly	Pro	Pro
				335					340					345
Arg	Lys	Lys	Pro	Gly	Leu	Ala	Ser	Phe	Arg	Leu	Ser	Gly	Leu	Lys
				350					355					360
Ser	Trp	Asp	Arg	Ala	Pro	Thr	Phe	Leu	Arg	Glu	Leu	Ser	Asp	Glu
				365					370					375
Thr	Val	Val	Leu	Gly	Gln	Ser	Val	Thr	Leu	Ala	Cys	Gln	Val	Ser
				380					385					390
Ala	Gln	Pro	Ala	Ala	Gln	Ala	Thr	Trp	Ser	Lys	Asp	Gly	Ala	Pro
				395					400					405
Leu	Glu	Ser	Ser	Ser	Arg	Val	Leu	Ile	Ser	Ala	Thr	Leu	Lys	Asn

Phe	Gln	Leu	Leu	410	Thr	Ile	Leu	Val	Val	415	Val	Ala	Glu	Asp	Leu	Gly	420
				425	Ser	Val	Ser	Asn	Ala	430	Leu	Gly	Thr	Val	Thr		435
Val	Tyr	Thr	Cys	440	Arg	Lys	Ala	Glu	Arg	445	Pro	Ser	Ser	Ser	Pro	Cys	450
Thr	Gly	Val	Leu	455	Glu	Val	Tyr	Ala	Asp	460	Gly	Val	Leu	Leu	Val	Trp	465
Pro	Asp	Ile	Gly	470	Ser	Tyr	Gly	Pro	Val	475	Thr	Tyr	Ile	Val	Gln	Cys	480
Lys	Pro	Val	Glu	485	Gly	Ser	Trp	Thr	Thr	490	Leu	Ala	Ser	Asp	Ile	Phe	495
Ser	Leu	Glu	Gly	500	Leu	Thr	Ser	Lys	Leu	505	Ser	Arg	Gly	Gly	Thr	Tyr	510
Asp	Cys	Cys	Tyr	515	Ala	Cys	Val	Ser	Lys	520	Ala	Gly	Met	Gly	Pro	Tyr	525
Thr	Phe	Arg	Thr	530	Glu	Gln	Val	Leu	Leu	535	Gly	Gly	Pro	Ser	His	Leu	540
Ser	Ser	Pro	Ser	545	Glu	Ser	Gln	Gly	Arg	550	Ser	Ala	Gln	Pro	Leu	Pro	555
Ala	Ser	Glu	Glu	560	Phe	Ala	Phe	Gln	Thr	565	Gln	Ile	Gln	Arg	Gly	Arg	570
Ser	Thr	Lys	Thr	575	Arg	Gln	Cys	Trp	Glu	580	Lys	Ala	Ser	Gly	Arg	Ala	585
Phe	Ser	Val	Val	590	Ile	Ile	Pro	Tyr	His	595	Pro	Lys	Asp	Lys	Thr	Ala	600
Leu	Ala	Ala	Lys	605	Tyr	Glu	Ala	Leu	Lys	610	Gly	Leu	Arg	His	Pro	His	615
Val	Leu	Arg	Glu	620	His	Ala	Ala	Tyr	Leu	625	Ser	Pro	Arg	His	Leu	Val	630
Leu	Ala	Gln	Leu	635	Leu	Cys	Ser	Gly	Pro	640	Glu	Leu	Leu	Pro	Cys	Leu	645
Leu	Ile	Leu	Glu	650	Ser	Tyr	Ser	Glu	Ser	655	Glu	Val	Lys	Asp	Tyr	Leu	660
Ala	Glu	Arg	Ala	665	Ser	Ala	Thr	Gln	Tyr	670	Leu	His	Asn	Gln	His	Ile	675
Trp	Gln	Met	Leu	680	Leu	Arg	Ser	Glu	Asn	685	Met	Ile	Ile	Thr	Glu	Tyr	690
Leu	His	Leu	Asp	695	Val	Val	Asp	Leu	Gly	700	Asn	Ala	Gln	Ser	Leu	Ser	705
Asn	Leu	Leu	Lys	710	Leu	Pro	Ser	Asp	Lys	715	Phe	Lys	Asp	Tyr	Leu	Glu	720
Gln	Glu	Lys	Val	725	Glu	Leu	Leu	Glu	Gly	730	Gln	Gly	Ala	Val	Pro	Gln	735
Thr	Met	Ala	Pro	740	Ala	Ile	Gly	Val	Thr	745	Ala	Phe	Ile	Met	Leu	Ser	750
Thr	Asp	Ile	Trp	755	Val	Ser	Ser	Glu	Gly	760	Ala	Arg	Asp	Leu	Gln	Arg	765
Ala	Glu	Tyr	Pro	770	Gly	Leu	Val	Arg	Leu	775	Ser	Arg	Cys	Tyr	Ala	Gly	780
Gly	Leu	Arg	Lys	785	Ala	Val	Ala	Phe	Leu	790	Arg	Ser	Thr	Leu	Cys	Ala	795
Leu	Ser	Gly	Gly	800	Arg	Pro	Cys	Ala	Ser	805	Ser	Cys	Leu	Gln	Cys	Pro	810
Gln	Pro	Trp	Gly	815	Glu	Gly	Pro	Ala	Cys	820	Ser	Arg	Pro	Ala	Pro	Val	825
Trp	Leu	Thr	Glu	830	Ala	Arg	Leu	Arg	Val	835	Phe	Val	Arg	Asn	Arg	Glu	840
Thr	Phe	Pro	Thr	845	Leu	Leu	Tyr	Lys	Arg	850	His	Asn	Leu	Ala	Gln	Val	855
Lys	Arg	Arg	Ala	860						865							870

Arg

<210> 21
 <211> 765
 <212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 063497CD1

<400> 21

Met	Ala	Gly	Phe	Lys	Arg	Gly	Tyr	Asp	Gly	Lys	Ile	Ala	Gly	Leu
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Tyr	Asp	Leu	Asp	Lys	Thr	Leu	Gly	Arg	Gly	His	Phe	Ala	Val	Val
				20					25					30
Lys	Leu	Ala	Arg	His	Val	Phe	Thr	Gly	Glu	Lys	Val	Ala	Val	Lys
				35					40					45
Val	Ile	Asp	Lys	Thr	Lys	Leu	Asp	Thr	Leu	Ala	Thr	Gly	His	Leu
				50					55					60
Phe	Gln	Glu	Val	Arg	Cys	Met	Lys	Leu	Val	Gln	His	Pro	Asn	Ile
				65					70					75
Val	Arg	Leu	Tyr	Glu	Val	Ile	Asp	Thr	Gln	Thr	Lys	Leu	Tyr	Leu
				80					85					90
Ile	Leu	Glu	Leu	Gly	Asp	Gly	Gly	Asp	Met	Phe	Asp	Tyr	Ile	Met
				95					100					105
Lys	His	Glu	Glu	Gly	Leu	Asn	Glu	Asp	Leu	Ala	Lys	Lys	Tyr	Phe
				110					115					120
Ala	Gln	Ile	Val	His	Ala	Ile	Ser	Tyr	Cys	His	Lys	Leu	His	Val
				125					130					135
Val	His	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Val	Val	Phe	Phe	Glu	Lys
				140					145					150
Gln	Gly	Leu	Val	Lys	Leu	Thr	Asp	Phe	Gly	Phe	Ser	Asn	Lys	Phe
				155					160					165
Gln	Pro	Gly	Lys	Lys	Leu	Thr	Thr	Ser	Cys	Gly	Ser	Leu	Ala	Tyr
				170					175					180
Ser	Ala	Pro	Glu	Ile	Leu	Leu	Gly	Asp	Glu	Tyr	Asp	Ala	Pro	Ala
				185					190					195
Val	Asp	Ile	Trp	Ser	Leu	Gly	Val	Ile	Leu	Phe	Met	Leu	Val	Cys
				200					205					210
Gly	Gln	Pro	Pro	Phe	Gln	Glu	Ala	Asn	Asp	Ser	Glu	Thr	Leu	Thr
				215					220					225
Met	Ile	Met	Asp	Cys	Lys	Tyr	Thr	Val	Pro	Ser	His	Val	Ser	Lys
				230					235					240
Glu	Cys	Lys	Asp	Leu	Ile	Thr	Arg	Met	Leu	Gln	Arg	Asp	Pro	Lys
				245					250					255
Arg	Arg	Ala	Ser	Leu	Glu	Glu	Ile	Glu	Asn	His	Pro	Trp	Leu	Gln
				260					265					270
Gly	Val	Asp	Pro	Ser	Pro	Ala	Thr	Lys	Tyr	Asn	Ile	Pro	Leu	Val
				275					280					285
Ser	Tyr	Lys	Asn	Leu	Ser	Glu	Glu	Glu	His	Asn	Ser	Ile	Ile	Gln
				290					295					300
Arg	Met	Val	Leu	Gly	Asp	Ile	Ala	Asp	Arg	Asp	Ala	Ile	Val	Glu
				305					310					315
Ala	Leu	Glu	Thr	Asn	Arg	Tyr	Asn	His	Ile	Thr	Ala	Thr	Tyr	Phe
				320					325					330
Leu	Leu	Ala	Glu	Arg	Ile	Leu	Arg	Glu	Lys	Gln	Glu	Lys	Glu	Ile
				335					340					345
Gln	Thr	Arg	Ser	Ala	Ser	Pro	Ser	Asn	Ile	Lys	Ala	Gln	Phe	Arg
				350					355					360
Gln	Ser	Trp	Pro	Thr	Lys	Ile	Asp	Val	Pro	Gln	Asp	Leu	Glu	Asp
				365					370					375
Asp	Leu	Thr	Ala	Thr	Pro	Leu	Ser	His	Ala	Thr	Val	Pro	Gln	Ser
				380					385					390
Pro	Ala	Arg	Ala	Ala	Asp	Ser	Val	Leu	Asn	Gly	His	Arg	Ser	Lys
				395					400					405
Gly	Leu	Cys	Asp	Ser	Ala	Lys	Lys	Asp	Asp	Leu	Pro	Glu	Leu	Ala
				410					415					420
Gly	Pro	Ala	Leu	Ser	Thr	Val	Pro	Pro	Ala	Ser	Leu	Lys	Pro	Thr
				425					430					435
Ala	Ser	Gly	Arg	Lys	Cys	Leu	Phe	Arg	Val	Glu	Glu	Asp	Glu	Glu
				440					445					450

Glu	Asp	Glu	Glu	Asp	Lys	Lys	Pro	Met	Ser	Leu	Ser	Thr	Gln	Val
				455					460					465
Val	Leu	Arg	Arg	Lys	Pro	Ser	Val	Thr	Asn	Arg	Leu	Thr	Ser	Arg
				470					475					480
Lys	Ser	Ala	Pro	Val	Leu	Asn	Gln	Ile	Phe	Glu	Glu	Gly	Glu	Ser
				485					490					495
Asp	Asp	Glu	Phe	Asp	Met	Asp	Glu	Asn	Leu	Pro	Pro	Lys	Leu	Ser
				500					505					510
Arg	Leu	Lys	Met	Asn	Ile	Ala	Ser	Pro	Gly	Thr	Val	His	Lys	Arg
				515					520					525
Tyr	His	Arg	Arg	Lys	Ser	Gln	Gly	Arg	Gly	Ser	Ser	Cys	Ser	Ser
				530					535					540
Ser	Glu	Thr	Ser	Asp	Asp	Asp	Ser	Glu	Ser	Arg	Arg	Arg	Leu	Asp
				545					550					555
Lys	Asp	Ser	Gly	Phe	Thr	Tyr	Ser	Trp	His	Arg	Arg	Asp	Ser	Ser
				560					565					570
Glu	Gly	Pro	Pro	Gly	Ser	Glu	Gly	Asp	Gly	Gly	Gly	Gln	Ser	Lys
				575					580					585
Pro	Ser	Asn	Ala	Ser	Gly	Gly	Val	Asp	Lys	Ala	Ser	Pro	Ser	Glu
				590					595					600
Asn	Asn	Ala	Gly	Gly	Gly	Ser	Pro	Ser	Ser	Gly	Ser	Gly	Gly	Asn
				605					610					615
Pro	Thr	Asn	Thr	Ser	Gly	Thr	Thr	Arg	Arg	Cys	Ala	Gly	Pro	Ser
				620					625					630
Asn	Ser	Met	Gln	Leu	Ala	Ser	Arg	Ser	Ala	Gly	Glu	Leu	Val	Glu
				635					640					645
Ser	Leu	Lys	Leu	Met	Ser	Leu	Cys	Leu	Gly	Ser	Gln	Leu	His	Gly
				650					655					660
Ser	Thr	Lys	Tyr	Ile	Ile	Asp	Pro	Gln	Asn	Gly	Leu	Ser	Phe	Ser
				665					670					675
Ser	Val	Lys	Val	Gln	Glu	Lys	Ser	Thr	Trp	Lys	Met	Cys	Ile	Ser
				680					685					690
Ser	Thr	Gly	Asn	Ala	Gly	Gln	Val	Pro	Ala	Val	Gly	Gly	Ile	Lys
				695					700					705
Phe	Phe	Ser	Asp	His	Met	Ala	Asp	Thr	Thr	Thr	Glu	Leu	Glu	Arg
				710					715					720
Ile	Lys	Ser	Lys	Asn	Leu	Lys	Asn	Asn	Val	Leu	Gln	Leu	Pro	Leu
				725					730					735
Cys	Glu	Lys	Thr	Ile	Ser	Val	Asn	Ile	Gln	Arg	Asn	Pro	Lys	Glu
				740					745					750
Gly	Leu	Leu	Cys	Ala	Ser	Ser	Pro	Ala	Ser	Cys	Cys	His	Val	Ile
				755					760					765

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<211> 588

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1625436CD1

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Leu	Phe	Glu	Glu	Leu	Gly	Lys	Gly	Ala	Phe	Ser	Val	Val	Arg	Arg
				20					25					30
Cys	Val	Lys	Lys	Thr	Ser	Thr	Gln	Glu	Tyr	Ala	Ala	Lys	Ile	Ile
				35					40					45
Asn	Thr	Lys	Lys	Leu	Ser	Ala	Arg	Asp	His	Gln	Lys	Leu	Glu	Arg
				50					55					60
Glu	Ala	Arg	Ile	Cys	Arg	Leu	Leu	Lys	His	Pro	Asn	Ile	Val	Arg
				65					70					75
Leu	His	Asp	Ser	Ile	Ser	Glu	Glu	Gly	Phe	His	Tyr	Leu	Val	Phe
				80					85					90
Asp	Leu	Val	Thr	Gly	Gly	Glu	Leu	Phe	Glu	Asp	Ile	Val	Ala	Arg

	95		100		105
Glu Tyr Tyr Ser	Glu Ala Asp Ala Ser	His Cys Ile His Gln	Ile		
	110		115		120
Leu Glu Ser Val	Asn His Ile His Gln	His Asp Ile Val His	Arg		
	125		130		135
Asp Leu Lys Pro	Glu Asn Leu Leu Leu	Ala Ser Lys Cys Lys	Gly		
	140		145		150
Ala Ala Val Lys	Leu Ala Asp Phe Gly	Leu Ala Ile Glu Val	Gln		
	155		160		165
Gly Glu Gln Gln	Ala Trp Phe Gly Phe	Ala Gly Thr Pro Gly	Tyr		
	170		175		180
Leu Ser Pro Glu	Val Leu Arg Lys Asp	Pro Tyr Gly Lys Pro	Val		
	185		190		195
Asp Ile Trp Ala	Cys Gly Val Ile Leu	Tyr Ile Leu Leu Val	Gly		
	200		205		210
Tyr Pro Pro Phe	Trp Asp Glu Asp Gln	His Lys Leu Tyr Gln	Gln		
	215		220		225
Ile Lys Ala Gly	Ala Tyr Asp Phe Pro	Ser Pro Glu Trp Asp	Thr		
	230		235		240
Val Thr Pro Glu	Ala Lys Asn Leu Ile	Asn Gln Met Leu Thr	Ile		
	245		250		255
Asn Pro Ala Lys	Arg Ile Thr Ala Asp	Gln Ala Leu Lys Tyr	Pro		
	260		265		270
Trp Val Cys Gln	Arg Ser Thr Val Ala	Ser Met Met His Arg	Gln		
	275		280		285
Glu Thr Val Glu	Cys Leu Arg Lys Phe	Asn Ala Arg Arg Lys	Leu		
	290		295		300
Lys Gly Ala Ile	Leu Thr Thr Met Leu	Val Ser Arg Asn Phe	Ser		
	305		310		315
Val Gly Arg Gln	Ser Ser Ala Pro Ala	Ser Pro Ala Ala Ser	Ala		
	320		325		330
Ala Gly Leu Ala	Gly Gln Ala Ala Lys	Ser Leu Leu Asn Lys	Lys		
	335		340		345
Ser Asp Gly Gly	Val Lys Lys Arg Lys	Ser Ser Ser Ser Val	His		
	350		355		360
Leu Met Pro Gln	Ser Asn Asn Lys Asn	Ser Leu Val Ser Pro	Ala		
	365		370		375
Gln Glu Pro Ala	Pro Leu Gln Thr Ala	Met Glu Pro Gln Thr	Thr		
	380		385		390
Val Val His Asn	Ala Thr Asp Gly Ile	Lys Gly Ser Thr Glu	Ser		
	395		400		405
Cys Asn Thr Thr	Thr Glu Asp Glu Asp	Leu Lys Ala Ala Pro	Leu		
	410		415		420
Arg Thr Gly Asn	Gly Ser Ser Val Pro	Glu Gly Arg Ser Ser	Arg		
	425		430		435
Asp Arg Thr Ala	Pro Ser Ala Gly Met	Gln Pro Gln Pro Ser	Leu		
	440		445		450
Cys Ser Ser Ala	Met Arg Lys Gln Glu	Ile Ile Lys Ile Thr	Glu		
	455		460		465
Gln Leu Ile Glu	Ala Ile Asn Asn Gly	Asp Phe Glu Ala Tyr	Thr		
	470		475		480
Lys Ile Cys Asp	Pro Gly Leu Thr Ser	Phe Glu Pro Glu Ala	Leu		
	485		490		495
Gly Asn Leu Val	Glu Gly Met Asp Phe	His Lys Phe Tyr Phe	Glu		
	500		505		510
Asn Leu Leu Ser	Lys Asn Ser Lys Pro	Ile His Thr Thr Ile	Leu		
	515		520		525
Asn Pro His Val	His Val Ile Gly Glu	Asp Ala Ala Cys Ile	Ala		
	530		535		540
Tyr Ile Arg Leu	Thr Gln Tyr Ile Asp	Gly Gln Gly Arg Pro	Arg		
	545		550		555
Thr Ser Gln Ser	Glu Glu Thr Arg Val	Trp His Arg Arg Asp	Gly		
	560		565		570
Lys Trp Leu Asn	Val His Tyr His Cys	Ser Gly Ala Pro Ala	Ala		
	575		580		585
Pro Leu Gln					

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<220>
 <221> misc_feature
 <223> Incyte ID No: 3330646CD1

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 Asp Arg Arg Glu Asp Gly Val Gln Arg Ala Ala Glu Leu Ser Gln
 20 25 30
 Ser Leu Pro Pro Arg Arg Arg Ala Pro Pro Gly Arg Gln Arg Leu
 35 40 45
 Glu Glu Arg Thr Gly Pro Ala Gly Pro Glu Gly Lys Glu Gln Asp
 50 55 60
 Val Ala Thr Gly Val Ser Pro Leu Leu Phe Arg Lys Leu Ser Asn
 65 70 75
 Pro Asp Ile Phe Ser Ser Thr Gly Lys Val Lys Leu Gln Arg Gln
 80 85 90
 Leu Ser Gln Asp Asp Cys Lys Leu Trp Arg Gly Asn Leu Ala Ser
 95 100 105
 Ser Leu Ser Gly Lys Gln Leu Leu Pro Leu Ser Ser Ser Val His
 110 115 120
 Ser Ser Val Gly Gln Val Thr Trp Gln Ser Ser Gly Glu Ala Ser
 125 130 135
 Asn Leu Val Arg Met Arg Asn Gln Ser Leu Gly Gln Ser Ala Pro
 140 145 150
 Ser Leu Thr Ala Gly Leu Lys Glu Leu Ser Leu Pro Arg Arg Gly
 155 160 165
 Ser Phe Cys Arg Thr Ser Asn Arg Lys Ser Leu Ile Val Thr Ser
 170 175 180
 Ser Thr Ser Pro Thr Leu Pro Arg Pro His Ser Pro Leu His Gly
 185 190 195
 His Thr Gly Asn Ser Pro Leu Asp Ser Pro Arg Asn Phe Ser Pro
 200 205 210
 Asn Ala Pro Ala His Phe Ser Phe Val Pro Ala Arg Arg Thr Asp
 215 220 225
 Gly Arg Arg Trp Ser Leu Ala Ser Leu Pro Ser Ser Gly Tyr Gly
 230 235 240
 Thr Asn Thr Pro Ser Ser Thr Val Ser Ser Ser Cys Ser Ser Gln
 245 250 255
 Glu Lys Leu His Gln Leu Pro Phe Gln Pro Thr Ala Asp Glu Leu
 260 265 270
 His Phe Leu Thr Lys His Phe Ser Thr Glu Ser Val Pro Asp Glu
 275 280 285
 Glu Gly Arg Gln Ser Pro Ala Met Arg Pro Arg Ser Arg Ser Leu
 290 295 300
 Ser Pro Gly Arg Ser Pro Val Ser Phe Asp Ser Glu Ile Ile Met
 305 310 315
 Met Asn His Val Tyr Lys Glu Arg Phe Pro Lys Ala Thr Ala Gln
 320 325 330
 Met Glu Glu Arg Leu Ala Glu Phe Ile Ser Ser Asn Thr Pro Asp
 335 340 345
 Ser Val Leu Pro Leu Ala Asp Gly Ala Leu Ser Phe Ile His His
 350 355 360
 Gln Val Ile Glu Met Ala Arg Asp Cys Leu Asp Lys Ser Arg Ser
 365 370 375
 Gly Leu Ile Thr Ser Gln Tyr Phe Tyr Glu Leu Gln Glu Asn Leu
 380 385 390
 Glu Lys Leu Leu Gln Asp Ala His Glu Arg Ser Glu Ser Ser Glu
 395 400 405
 Val Ala Phe Val Met Gln Leu Val Lys Lys Leu Met Ile Ile Ile
 410 415 420
 Ala Arg Pro Ala Arg Leu Leu Glu Cys Leu Glu Phe Asp Pro Glu

	425		430		435
Glu Phe Tyr His	Leu Leu Glu Ala Ala	Glu Gly His Ala Lys	Glu		
	440		445		450
Gly Gln Gly Ile	Lys Cys Asp Ile Pro	Arg Tyr Ile Val Ser	Gln		
	455		460		465
Leu Gly Leu Thr	Arg Asp Pro Leu Glu	Glu Met Ala Gln Leu	Ser		
	470		475		480
Ser Cys Asp Ser	Pro Asp Thr Pro Glu	Thr Asp Asp Ser Ile	Glu		
	485		490		495
Gly His Gly Ala	Ser Leu Pro Ser Lys	Lys Thr Pro Ser Glu	Glu		
	500		505		510
Asp Phe Glu Thr	Ile Lys Leu Ile Ser	Asn Gly Ala Tyr Gly	Ala		
	515		520		525
Val Phe Leu Val	Arg His Lys Ser Thr	Arg Gln Arg Phe Ala	Met		
	530		535		540
Lys Lys Ile Asn	Lys Gln Asn Leu Ile	Leu Arg Asn Gln Ile	Gln		
	545		550		555
Gln Ala Phe Val	Glu Arg Asp Ile Leu	Thr Phe Ala Glu Asn	Pro		
	560		565		570
Phe Val Val Ser	Met Phe Cys Ser Phe	Asp Thr Lys Arg His	Leu		
	575		580		585
Cys Met Val Met	Glu Tyr Val Glu Gly	Gly Asp Cys Ala Thr	Leu		
	590		595		600
Leu Lys Asn Ile	Gly Ala Leu Pro Val	Asp Met Val Arg Leu	Tyr		
	605		610		615
Phe Ala Glu Thr	Val Leu Ala Leu Glu	Tyr Leu His Asn Tyr	Gly		
	620		625		630
Ile Val His Arg	Asp Leu Lys Pro Asp	Asn Leu Leu Ile Thr	Ser		
	635		640		645
Met Gly His Ile	Lys Leu Thr Asp Phe	Gly Leu Ser Lys Met	Gly		
	650		655		660
Leu Met Ser Leu	Thr Thr Asn Leu Tyr	Glu Gly His Ile Glu	Lys		
	665		670		675
Asp Ala Arg Glu	Phe Leu Asp Lys Gln	Val Cys Gly Thr Pro	Glu		
	680		685		690
Tyr Ile Ala Pro	Glu Val Ile Leu Arg	Gln Gly Tyr Gly Lys	Pro		
	695		700		705
Val Asp Trp Trp	Ala Met Gly Ile Ile	Leu Tyr Glu Phe Leu	Val		
	710		715		720
Gly Cys Val Pro	Phe Phe Gly Asp Thr	Pro Glu Glu Leu Phe	Gly		
	725		730		735
Gln Val Ile Ser	Asp Glu Ile Val Trp	Pro Glu Gly Asp Glu	Ala		
	740		745		750
Leu Pro Pro Asp	Ala Gln Asp Leu Thr	Ser Lys Leu Leu His	Gln		
	755		760		765
Asn Pro Leu Glu	Arg Leu Gly Thr Gly	Ser Ala Tyr Glu Val	Lys		
	770		775		780
Gln His Pro Phe	Phe Thr Gly Leu Asp	Trp Thr Gly Leu Leu	Arg		
	785		790		795
Gln Lys Ala Glu	Phe Ile Pro Gln Leu	Glu Ser Glu Asp Asp	Thr		
	800		805		810
Ser Tyr Phe Asp	Thr Arg Ser Glu Arg	Tyr His His Met Asp	Ser		
	815		820		825
Glu Asp Glu Glu	Glu Val Ser Glu Asp	Gly Cys Leu Glu Ile	Arg		
	830		835		840
Gln Phe Ser Ser	Cys Ser Pro Arg Phe	Asn Lys Val Tyr Ser	Ser		
	845		850		855
Met Glu Arg Leu	Ser Leu Leu Glu Glu	Arg Arg Thr Pro Pro	Pro		
	860		865		870
Thr Lys Arg Ser	Leu Ser Glu Glu Lys	Glu Asp His Ser Asp	Gly		
	875		880		885
Leu Ala Gly Leu	Lys Gly Arg Asp Arg	Ser Trp Val Ile Gly	Ser		
	890		895		900
Pro Glu Ile Leu	Arg Lys Arg Leu Ser	Val Ser Glu Ser Ser	His		
	905		910		915
Thr Glu Ser Asp	Ser Ser Pro Pro Met	Thr Val Arg Arg Arg	Cys		
	920		925		930

Ser	Gly	Leu	Leu	Asp	Ala	Pro	Arg	Phe	Pro	Glu	Gly	Pro	Glu	Glu
				935					940					945
Ala	Ser	Ser	Thr	Leu	Arg	Arg	Gln	Pro	Gln	Glu	Gly	Ile	Trp	Val
				950					955					960
Leu	Thr	Pro	Pro	Ser	Gly	Glu	Gly	Val	Ser	Gly	Pro	Val	Thr	Glu
				965					970					975
His	Ser	Gly	Glu	Gln	Arg	Pro	Lys	Leu	Asp	Glu	Glu	Ala	Val	Gly
				980					985					990
Arg	Ser	Ser	Gly	Ser	Ser	Pro	Ala	Met	Glu	Thr	Arg	Gly	Arg	Gly
				995					1000					1005
Thr	Ser	Gln	Leu	Ala	Glu	Gly	Ala	Thr	Ala	Lys	Ala	Ile	Ser	Asp
				1010					1015					1020
Leu	Ala	Val	Arg	Arg	Ala	Arg	His	Arg	Leu	Leu	Ser	Gly	Asp	Ser
				1025					1030					1035
Thr	Glu	Lys	Arg	Thr	Ala	Arg	Pro	Val	Asn	Lys	Val	Ile	Lys	Ser
				1040					1045					1050
Ala	Ser	Ala	Thr	Ala	Leu	Ser	Leu	Leu	Ile	Pro	Ser	Glu	His	His
				1055					1060					1065
Thr	Cys	Ser	Pro	Leu	Ala	Ser	Pro	Met	Ser	Pro	His	Ser	Gln	Ser
				1070					1075					1080
Ser	Asn	Pro	Ser	Ser	Arg	Asp	Ser	Ser	Pro	Ser	Arg	Asp	Phe	Leu
				1085					1090					1095
Pro	Ala	Leu	Gly	Ser	Met	Arg	Pro	Pro	Ile	Ile	Ile	His	Arg	Ala
				1100					1105					1110
Gly	Lys	Lys	Tyr	Gly	Phe	Thr	Leu	Arg	Ala	Ile	Arg	Val	Tyr	Met
				1115					1120					1125
Gly	Asp	Ser	Asp	Val	Tyr	Thr	Val	His	His	Met	Val	Trp	His	Val
				1130					1135					1140
Glu	Asp	Gly	Gly	Pro	Ala	Ser	Glu	Ala	Gly	Leu	Arg	Gln	Gly	Asp
				1145					1150					1155
Leu	Ile	Thr	His	Val	Asn	Gly	Glu	Pro	Val	His	Gly	Leu	Val	His
				1160					1165					1170
Thr	Glu	Val	Val	Glu	Leu	Ile	Leu	Lys	Ser	Gly	Asn	Lys	Val	Ala
				1175					1180					1185
Ile	Ser	Thr	Thr	Pro	Leu	Glu	Asn	Thr	Ser	Ile	Lys	Val	Gly	Pro
				1190					1195					1200
Ala	Arg	Lys	Gly	Ser	Tyr	Lys	Ala	Lys	Met	Ala	Arg	Arg	Ser	Lys
				1205					1210					1215
Arg	Ser	Arg	Gly	Lys	Asp	Gly	Gln	Glu	Ser	Arg	Lys	Arg	Ser	Ser
				1220					1225					1230
Leu	Phe	Arg	Lys	Ile	Thr	Lys	Gln	Ala	Ser	Leu	Leu	His	Thr	Ser
				1235					1240					1245
Arg	Ser	Leu	Ser	Ser	Leu	Asn	Arg	Ser	Leu	Ser	Ser	Gly	Glu	Ser
				1250					1255					1260
Gly	Pro	Gly	Ser	Pro	Thr	His	Ser	His	Ser	Leu	Ser	Pro	Arg	Ser
				1265					1270					1275
Pro	Thr	Gln	Gly	Tyr	Arg	Val	Thr	Pro	Asp	Ala	Val	His	Ser	Val
				1280					1285					1290
Gly	Gly	Asn	Ser	Ser	Gln	Ser	Ser	Ser	Pro	Ser	Ser	Ser	Val	Pro
				1295					1300					1305
Ser	Ser	Pro	Ala	Gly	Ser	Gly	His	Thr	Arg	Pro	Ser	Ser	Leu	His
				1310					1315					1320
Gly	Leu	Ala	Pro	Lys	Leu	Gln	Arg	Gln	Tyr	Arg	Ser	Pro	Arg	Arg
				1325					1330					1335
Lys	Ser	Ala	Gly	Ser	Ile	Pro	Leu	Ser	Pro	Leu	Ala	His	Thr	Pro
				1340					1345					1350
Ser	Pro	Pro	Pro	Pro	Thr	Ala	Ser	Pro	Gln	Arg	Ser	Pro	Ser	Pro
				1355					1360					1365
Leu	Ser	Gly	His	Val	Ala	Gln	Ala	Phe	Pro	Thr	Lys	Leu	His	Leu
				1370					1375					1380
Ser	Pro	Pro	Leu	Gly	Arg	Gln	Leu	Ser	Arg	Pro	Lys	Ser	Ala	Glu
				1385					1390					1395
Pro	Pro	Arg	Ser	Pro	Leu	Leu	Lys	Arg	Val	Gln	Ser	Ala	Glu	Lys
				1400					1405					1410
Leu	Ala	Ala	Ala	Leu	Ala	Ala	Ser	Glu	Lys	Lys	Leu	Ala	Thr	Ser
				1415					1420					1425
Arg	Lys	His	Ser	Leu	Asp	Leu	Pro	His	Ser	Glu	Leu	Lys	Lys	Glu

1430	1435	1440
Leu Pro Pro Arg Glu Val Ser Pro Leu Glu Val Val Gly Ala Arg		
1445	1450	1455
Ser Val Leu Ser Gly Lys Gly Ala Leu Pro Gly Lys Gly Val Leu		
1460	1465	1470
Gln Pro Ala Pro Ser Arg Ala Leu Gly Thr Leu Arg Gln Asp Arg		
1475	1480	1485
Ala Glu Arg Arg Glu Ser Leu Gln Lys Gln Glu Ala Ile Arg Glu		
1490	1495	1500
Val Asp Ser Ser Glu Asp Asp Thr Glu Glu Gly Pro Glu Asn Ser		
1505	1510	1515
Gln Gly Ala Gln Glu Leu Ser Leu Ala Pro His Pro Glu Val Ser		
1520	1525	1530
Gln Ser Val Ala Pro Lys Gly Ala Gly Glu Ser Gly Glu Glu Asp		
1535	1540	1545
Pro Phe Pro Ser Arg Asp Pro Arg Ser Leu Gly Pro Met Val Pro		
1550	1555	1560
Ser Leu Leu Thr Gly Ile Thr Leu Gly Pro Pro Arg Met Glu Ser		
1565	1570	1575
Pro Ser Gly Pro His Arg Arg Leu Gly Ser Pro Gln Ala Ile Glu		
1580	1585	1590
Glu Ala Ala Ser Ser Ser Ser Ala Gly Pro Asn Leu Gly Gln Ser		
1595	1600	1605
Gly Ala Thr Asp Pro Ile Pro Pro Glu Gly Cys Trp Lys Ala Gln		
1610	1615	1620
His Leu His Thr Gln Ala Leu Thr Ala Leu Ser Pro Ser Thr Ser		
1625	1630	1635
Gly Leu Thr Pro Thr Ser Ser Cys Ser Pro Pro Ser Ser Thr Ser		
1640	1645	1650
Gly Lys Leu Ser Met Trp Ser Trp Lys Ser Leu Ile Glu Gly Pro		
1655	1660	1665
Asp Arg Ala Ser Pro Ser Arg Lys Ala Thr Met Ala Gly Gly Leu		
1670	1675	1680
Ala Asn Leu Gln Asp Leu Glu Asn Thr Thr Pro Ala Gln Pro Lys		
1685	1690	1695
Asn Leu Ser Pro Arg Glu Gln Gly Lys Thr Gln Pro Pro Ser Ala		
1700	1705	1710
Pro Arg Leu Ala His Pro Ser Tyr Glu Asp Pro Ser Gln Gly Trp		
1715	1720	1725
Leu Trp Glu Ser Glu Cys Ala Gln Ala Val Lys Glu Asp Pro Ala		
1730	1735	1740
Leu Ser Ile Thr Gln Val Pro Asp Ala Ser Gly Asp Arg Arg Gln		
1745	1750	1755
Asp Val Pro Cys Arg Gly Cys Pro Leu Thr Gln Lys Ser Glu Pro		
1760	1765	1770
Ser Leu Arg Arg Gly Gln Glu Pro Gly Gly His Gln Lys His Arg		
1775	1780	1785
Asp Leu Ala Leu Val Pro Asp Glu Leu Leu Lys Gln Thr		
1790	1795	

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<211> 362

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3562763CD1

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Arg Arg Arg Pro Glu Gly Gly Gly Gly Ser Ala Arg Pro Arg Tyr	
20 25 30	
Ser Leu Leu Ala Glu Ile Gly Arg Gly Ser Tyr Gly Val Val Tyr	
35 40 45	
Glu Ala Val Ala Gly Arg Ser Gly Ala Arg Val Ala Val Lys Lys	

				50					55					60
Ile	Arg	Cys	Asp	Ala	Pro	Glu	Asn	Val	Glu	Leu	Ala	Leu	Ala	Glu
				65					70					75
Phe	Trp	Ala	Leu	Thr	Ser	Leu	Lys	Arg	Arg	His	Gln	Asn	Val	Val
				80					85					90
Gln	Phe	Glu	Glu	Cys	Val	Leu	Gln	Arg	Asn	Gly	Leu	Ala	Gln	Arg
				95					100					105
Met	Ser	His	Gly	Asn	Lys	Ser	Ser	Gln	Leu	Tyr	Leu	Arg	Leu	Val
				110					115					120
Glu	Thr	Ser	Leu	Lys	Gly	Glu	Arg	Ile	Leu	Gly	Tyr	Ala	Glu	Glu
				125					130					135
Pro	Cys	Tyr	Leu	Trp	Phe	Val	Met	Glu	Phe	Cys	Glu	Gly	Gly	Asp
				140					145					150
Leu	Asn	Gln	Tyr	Val	Leu	Ser	Arg	Arg	Pro	Asp	Pro	Ala	Thr	Asn
				155					160					165
Lys	Ser	Phe	Met	Leu	Gln	Leu	Thr	Ser	Ala	Ile	Ala	Phe	Leu	His
				170					175					180
Lys	Asn	His	Ile	Val	His	Arg	Asp	Leu	Lys	Pro	Asp	Asn	Ile	Leu
				185					190					195
Ile	Thr	Glu	Arg	Ser	Gly	Thr	Pro	Ile	Leu	Lys	Val	Ala	Asp	Phe
				200					205					210
Gly	Leu	Ser	Lys	Val	Cys	Ala	Gly	Leu	Ala	Pro	Arg	Gly	Lys	Glu
				215					220					225
Gly	Asn	Gln	Asp	Asn	Lys	Asn	Val	Asn	Val	Asn	Lys	Tyr	Trp	Leu
				230					235					240
Ser	Ser	Ala	Cys	Gly	Ser	Asp	Phe	Tyr	Met	Ala	Pro	Glu	Val	Trp
				245					250					255
Glu	Gly	His	Tyr	Thr	Ala	Lys	Ala	Asp	Ile	Phe	Ala	Leu	Gly	Ile
				260					265					270
Ile	Ile	Trp	Ala	Met	Ile	Glu	Arg	Ile	Thr	Phe	Ile	Asp	Ser	Glu
				275					280					285
Thr	Lys	Lys	Glu	Leu	Leu	Gly	Thr	Tyr	Ile	Lys	Gln	Gly	Thr	Glu
				290					295					300
Ile	Val	Pro	Val	Gly	Glu	Ala	Leu	Leu	Glu	Asn	Pro	Lys	Met	Glu
				305					310					315
Leu	His	Ile	Pro	Gln	Lys	Arg	Arg	Thr	Ser	Met	Ser	Glu	Gly	Ile
				320					325					330
Lys	Gln	Leu	Leu	Lys	Asp	Met	Leu	Ala	Ala	Asn	Pro	Gln	Asp	Arg
				335					340					345
Pro	Asp	Ala	Phe	Glu	Leu	Glu	Thr	Arg	Met	Asp	Gln	Val	Thr	Cys
				350					355					360
Ala	Ala													

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<211> 275

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 621293CD1

<400> 25

Met	Val	Pro	Glu	Asp	Ile	Ser	Glu	Leu	Glu	Thr	Ala	Gln	Lys	Leu
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Leu	Glu	Tyr	His	Arg	Asn	Ile	Val	Arg	Val	Ile	Pro	Ser	Tyr	Pro
				20					25					30
Lys	Ile	Leu	Lys	Val	Ile	Ser	Ala	Asp	Gln	Pro	Cys	Val	Asp	Val
				35					40					45
Phe	Tyr	Gln	Ala	Leu	Thr	Tyr	Val	Gln	Ser	Asn	His	Arg	Thr	Asn
				50					55					60
Ala	Pro	Phe	Thr	Pro	Arg	Val	Leu	Leu	Leu	Gly	Pro	Val	Gly	Ser
				65					70					75
Gly	Lys	Ser	Leu	Gln	Ala	Ala	Leu	Leu	Ala	Gln	Lys	Tyr	Arg	Leu
				80					85					90
Val	Asn	Val	Cys	Cys	Gly	Gln	Leu	Leu	Lys	Glu	Ala	Val	Ala	Asp

	95		100		105
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Met Ala Val Pro	Asp Ser Leu Leu Met	Lys Val Leu Ser Gln	Arg		
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Leu Asp Gln Gln	Asp Cys Ile Gln Lys	Gly Trp Val Leu His	Gly		
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Val Pro Arg Asp	Leu Asp Gln Ala His	Leu Leu Asn Arg Leu	Gly		
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Tyr Asn Pro Asn	Arg Val Phe Phe Leu	Asn Val Pro Phe Asp	Ser		
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Ile Met Glu Arg	Leu Thr Leu Arg Arg	Ile Asp Pro Val Thr	Gly		
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Glu Arg Tyr His	Leu Met Tyr Lys Pro	Pro Pro Thr Met Glu	Ile		
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Gln Ala Arg Leu	Leu Gln Asn Pro Lys	Asp Ala Glu Glu Gln	Val		
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Lys Leu Lys Met	Asp Leu Phe Tyr Arg	Asn Ser Ala Asp Leu	Glu		
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Gln Leu Tyr Gly	Ser Ala Ile Thr Leu	Asn Gly Asp Gln Asp	Pro		
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Ser Glu Pro Glu Arg	Ala Gly Leu Gly Pro	Ala Pro Gly Thr Glu	
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Ser Pro Gln Ala Glu	Phe Trp Thr Asp Gly	Gln Thr Glu Pro Ala	
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Ala Ala Gly Leu Gly	Val Glu Thr Glu Arg	Pro Lys Gln Lys Thr	
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Glu Pro Asp Arg Ser	Ser Leu Arg Thr His	Leu Glu Trp Ser Trp	
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Thr Glu Leu Glu Thr	His Gly Ser Gln Thr	Gln Pro Glu Arg Val	
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Lys Ser Trp Ala Asp	Asn Leu Trp Thr His	Gln Asn Ser Ser Ser	
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Gly Glu Leu Leu	275	Thr His Leu Tyr Ser	280	His Leu Lys Cys Ser	285
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<213> Homo sapiens

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<220>

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<223> Incyte ID No: 3951059CB1

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<211> 1689

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<223> Incyte ID No: 7472822CB1

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<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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<223> a, t, c, g, or other

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<211> 1662

<212> DNA

<213> Homo sapiens

<220>

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<223> Incyte ID No: 7477204CB1

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<211> 3225

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<223> Incyte ID No: 3016969CB1

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